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(71) Applicant *(for all designated States except US)*: **HUMAN GENOME SCIENCES, INC.** [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **BIRSE, Charles, E.** [GB/US]; 13822 Saddleview Drive, North Potomac, MD 20878 (US). **ROSEN, Craig, A.** [US/US]; 22400 Rolling Hill Road, Laytonsville, MD 20882 (US).

(74) Agents: **WALES, Michele, M.** et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).

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(54) Title: NUCLEIC ACIDS, PROTEINS, AND ANTIBODIES

(57) Abstract: The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Nucleic Acids, Proteins, and Antibodies

This application refers to a "Sequence Listing" that is provided on electronic media in computer readable form pursuant to Administrative Instructions Section 801(a)(i) and as a paper copy. The Sequence Listing forms a part of this description pursuant to Rule 5.2 and Administrative Instructions Sections 801 to 806, and is hereby incorporated in its entirety.

The Sequence Listing is provided as an electronic file (PA131PCTSL..txt, 5,210,863 bytes in size, created on May 18, 2001) on three identical compact discs (CD-R), labeled "COPY 1," "COPY 2," and "CRF." The Sequence Listing complies with Annex C of the Administrative Instructions, and may be viewed, for example, on an IBM-PC machine running the MS-Windows operating system by using the V viewer software, version 2000 (see World Wide Web URL: http://www.fileviewer.com).

Field of the Invention

[0001] The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Background of the Invention

[0002] Protein transport is a quintessential process for both prokaryotic and eukaryotic cells. Transport of an individual protein usually occurs via an amino-terminal signal sequence, which directs, or targets, the protein from its ribosomal assembly site to a particular cellular or extracellular location. Transport may involve any combination of several of the following steps: contact with a chaperone, unfolding, interaction with a receptor and/or a pore complex, addition of energy, and refolding. Moreover, an

extracellular protein may be produced as an inactive precursor. Once the precursor has been exported, removal of the signal sequence by a signal peptidase activates the protein.

[0003] Although amino-terminal signal sequences vary substantially, many patterns and overall properties are shared. Recently, hidden Markov models (HMMs), statistical alternatives to FASTA and Smith Waterman algorithms, have been used to find shared patterns, specifically consensus sequences (Pearson, W.R. and D.J. Lipman PNAS 85:2444-48 (1988); Smith, T.F. and M.S. Waterman J. Mol. Biol. 147:195-97 (1981)). Although they were initially developed to examine speech recognition patterns, HMMs have been used in biology to analyze protein and DNA sequences and to model protein structure (Krogh, A. et al. J. Mol. Biol. 235:1501-31 (1994); Collin, M. et al. Protein Sci. 2:305-14 (1993)). HMMs have a formal probabilistic basis and use position-specific scores for amino acids or nucleotides and for opening and extending an insertion or deletion. The algorithms are quite flexible in that they incorporate information from newly identified sequences to build even more successful patterns. Other methods exist to identify membrane associated proteins. Klein et al. have developed a method ("ALOM", also called as KKD) to detect potential transmembrane segments in polypeptides (Klein, P. et al. Biochim. Biophys. Acta, 815:468 (1985)). It attempts to identify the most probable transmembrane segment from the average hydrophobicity value over a range of amino acid residues. It predicts whether the segment is a transmembrane segment (INTEGRAL) or not (PERIPHERAL) and thus, can suggest membrane association of a polypeptide.

[0004] Some examples of the protein families which are known to be plasma membrane associated are receptors (nuclear, 4 transmembrane, G protein coupled, and tyrosine kinase), cytokines (chemokines), hormones (growth and differentiation factors), neuropeptides and vasomediators, protein kinases, phosphatases, phospholipases, phosphodiesterases, nucleotide cyclases, matrix molecules (adhesion, cadherin, extracellular matrix molecules, integrin, and selectin), seven transmembrane receptors, ion channels (calcium, chloride, potassium, and sodium), proteases, transporter/pumps (amino acid, protein, sugar, metal and vitamin; calcium, phosphate, potassium, and sodium) and regulatory proteins. Descriptions of some of these proteins (seven transmembrane receptors, kinases, matrix proteins, fibronectins, defensins, EF-hand domain containing

proteins, mac/perforin family members, pancreatic hormones, serine carboxypeptidases, tumor necrosis factors (TNFs)) and diseases associated with their dysfunction follow.

Seven transmembrane receptors-

[0005] The seven transmembrane receptors (also known as heptahelical, serpentine, or G protein-coupled receptors) comprise a superfamily of structurally related molecules. Possible relationships among seven transmembrane receptors (7TM receptors) for which amino acid sequence had previously been reported are reviewed in Probst et al., *DNA and Cell Biology*, 11(1):1-20 (1992). Briefly, the 7TM receptors exhibit detectable amino acid sequence similarity and all appear to share a number of structural characteristics including: an extracellular amino terminus; seven predominantly hydrophobic α-helical domains (of about 20-30 amino acids) which are believed to span the cell membrane and are referred to as transmembrane domains TM 1-7; approximately twenty well-conserved amino acids; and a cytoplasmic carboxy terminus.

[0006] Each 7TM receptor is predicted to associate with a particular G protein at the intracellular surface of the plasma membrane. The binding of the receptor to its ligand is thought to result in activation (i.e., the exchange of GTP for GDP on the α-subunit) of the G protein which in turn stimulates specific intracellular signal-transducing enzymes and channels. Thus, the function of each 7TM receptor is to discriminate its specific ligand from the complex extracellular milieu and then to activate G proteins to produce a specific intracellular signal. Transmembrane domain-3 (TM3) is believed to be essential in signal transduction (Cotecchia et al., *Proc. Natl. Acad. Sci.*, USA, 87:2896-2900 (1990)). Other regions may be essential for biological activity as well (Lefkowitz, *Nature*, 265:603-604 (1993)).

[0007] Mutations in the third intracellular loop of one 7TM receptor (the thyrotropin receptor) and in the adjacent sixth transmembrane domain of another 7TM receptor (the luteinizing hormone receptor) have been reported to be the genetic defects responsible for an uncommon form of hyperthyroidism (Parma et al., *Nature*, 365:649-651 (1993) and for familial precocious puberty (Shenker et al., *Nature*, 365:652-654 (1993)), respectively. In both cases the mutations result in constitutive activation of the G protein receptors. Other studies have shown that mutations that prevent the activation of 7TM receptors are responsible for states of hormone resistance which are responsible for diseases such as

congenital nephrogenic diabetes insipidus. See Rosenthal et al., *J. Biol. Chem.*, 268:13030-13033 (1993). Still other studies have shown that several 7TM receptors can function as protooncogenes and be activated by mutational alteration. See, for example, Allen et al., *Proc. Natl. Acad. Sci. USA*, 88:11354-11358 (1991) which suggests that spontaneously occurring mutations in some 7TM receptors may alter the normal function of the receptors and result in uncontrolled cell growth associated with human disease states such as neoplasia and atherosclerosis. Therefore, mutations in 7TM receptors may underlie a number of human pathologies.

Kinases-

[0008] The kinases comprise the largest known group of proteins, a superfamily of enzymes with widely varied fimctions and specificities. Kinases regulate many different cell proliferation, differentiation, and signaling processes by adding phosphate groups to proteins. Receptor mediated extracellular events trigger the transfer of these high energy phosphate groups and activate intracellular signaling cascades. Activation is roughly analogous to the turning on a molecular switch, and in cases where signalling is uncontrolled, may be associated with or produce inflammation and cancer.

[0009] Almost all kinases contain a similar 250-300 amino acid catalytic domain. The N-terminal domain, which contains subdomains I-IV, generally folds into a two-lobed structure which binds and orients the ATP (or GTP) donor molecule. The larger C terminal lobe, which contains subdomains VIA-XI, binds the protein substrate and carries out the transfer of the gamma phosphate from ATP to the hydroxyl group of a serine, threonine, or tyrosine residue. Subdomain V spans the two lobes.

[0010] The kinases may be categorized into families by the different amino acid sequences (between 5 and 100 residues) located on either side of, or inserted into loops of, the kinase domain. These amino acid sequences allow the regulation of each kinase as it recognizes and interacts with its target protein. The primary structure of the kinase domain is conserved and contains specific residues and identifiable motifs or patterns of amino acids. The serine threonine kinases represent one family which preferentially phosphorylates serine or threonine residues. Many serine threonine kinases, including those from human, rabbit, rat, mouse, and chicken cells and tissues, have been described

(Hardie, G. and Hanks, S. (1995) The Protein Kinase Facts Books, Vol 1:7-20 Academic Press, San Diego, CA).

Matrix Proteins-

[0011] The matrix proteins (MPs) provide structural support, cell and tissue identity, and autocrine, paracrine and juxtacrine properties for most eukaryotic cells (McGowan, S.E. (1992) FASEB J. 6:2895-2904). MPs include adhesion molecules, integrins and selectins, cadherins, lectins, lipocalins, and extracellular matrix proteins (ECMs). MPs possess many different domains which interact with soluble, extracellular molecules. These domains include collagen-like domains, EGF-like domains, immunoglobulin-like domains, fibronectin-like domains, type A domain of von Willebrand factor (vWFA)-like modules, ankyrin repeat modules, RDG or RDG-like sequences, carbohydrate-binding domains, and calcium-binding domains.

[0012] The diversity, distribution and biochemistry of MPs is indicative of their many, overlapping roles in cell proliferation and cell signaling. MPs function in the formation, growth, remodeling, and maintenance of bone, and in the mediation and regulation of inflammation. Biochemical changes that result from congenital, epigenetic, or infectious diseases affect the expression and balance of MPs. This balance, in turn, affects the activation, proliferation, differentiation, and migration of leukocytes and determines whether the immune response is appropriate or self-destructive (Roman, J. (1996) Immunol. Res. 15:163-178).

Fibronectins-

[0013] Fibronectin proteins play a vital role in the structure and function of the extracellular matrix (ECM). Defects in the function of the ECM are thought to be involved in diseases such as osteoporosis, atherosclerosis, arthritis, and fibrotic diseases. Fibronectin enables cells to adhere to the ECM, and influences the growth and migration of cells as well as the organization of the cytoskeleton. As a major component of the ECM, Fibronectin is thought to influence such processes as cellular adhesion and migration, particularly during development, as well as processes such as wound repair (R.O. Hynes, *PNAS*, 96:2588-90 (1999)).

[0014] Fibronectin is a disulfide-linked dimeric glycoprotein composed of type I, type II, and type III fibronectin repeats. Type I repeats are approximately 45 amino acids in length and are located at the amino- and carboxy-termini of the protein. Type II domains are approximately 40-60 amino acids in length, and contain four conserved cysteines involved in disulfide bonding. It is thought that the type II domains may function in collagen binding. There are approximately 15-17 type III domains, arranged in tandem in the middle of the protein, that are thought to provide elasticity to fibronectin.

Defensins-

[0015] Mammalian defensins are produced by the epidermis and mucosal epithelium as innate effector molecules thought to function in an antimicrobial capacity. Defensins are cytotoxic peptides with a broad range of activity on gram-positive and negative bacteria, fungi, parasites, viruses, and mycobacteria. The two characterized defensins are the alpha and beta defensins. The alpha-defensins are produced by neutrophils and macrophage, while the beta-defensins are produced by epithelia (Singh, P.K., et al., *PNAS*, 95:14961-66 (1998); Lillard, J.W., et al., *PNAS*, 96:651-56 (1999)).

[0016] Defensin peptides range in length from approximately 29 to 35 amino acids, and include six conserved cysteine residues involved in disulfide bond formation and protein folding. The distribution and connection of the cysteine residues differs between the alpha and beta defensins.

EF-hand domain containing proteins-

[0017] Calcium is well known to be essential for cell signaling. However, calcium also plays a role in such cellular processes as protein processing and membrane traffic to and through the Golgi. Many proteins thought to be involved in the binding of calcium accomplish this in part through a protein calcium-binding domain known as the EF-hand domain.

[0018] The domain consists of a twelve residue loop flanked by a twelve residue alpha-helical domain on both sides. In the EF hand loop, the calcium ion is situated in a coordinated pentagonal bipyramidal configuration. An invariant Glutamic acid or Aspartic acid residue provides two oxygens for liganding the calcium ion.

[0019] Proteins containing this domain include aequorin and Renilla luciferin binding protein (LBP), Recoverins, Calmodulin, Calpain small and large chains, Calretinin, Calcyclin, Fimbrin, Serine/Threonine protein phosphatase, and Diacylglycerol kinase, for example.

MAC/Perforin Family Members-

[0020] The Membrane Attack Complex (MAC) is one of the sequentially activated, membrane bound complexes of the complement system used to eliminate diseased or non-compliant cells. Under this system, activated C5b sequentially binds C6 and C7, which insert into cell membranes. This complex then binds one molecule of C8, followed by between 1 and 18 molecules of C9, which polymerizes to generate a transmembrane channel. These transmembrane channels pierce the membrane, increasing the cell's permeability. These channels permit small molecules in the cell to exchange with the medium. Therefore, water is osmotically drawn into the cell, eventually resulting in the cell bursting.

[0021] Similarly, Perforin is a molecule produced by cytotoxic T cells. In the presence of calcium, Perforin polymerizes into transmembrane channels capable of lysing a variety of target cells in a nonspecific manner.

Pancreatic Hormones- Serine Carboxypeptidases-

[0022] Pancreatic hormone (PP) is a peptide of approximately 80 amino acids in length that is generated in pancreatic islets of Langherhans and consequently secreted. Pancreatic hormone is thought to function as a regulator of pancreatic and gastrointestinal functions.

[0023] Representative members of the pancreatic hormones family of proteins include Neuropeptide Y, Peptide YY, and skin peptide YY. These proteins may be useful as therapeutics for controlling secretion of the gonadotropin-releasing hormone, disorders related to feeding, vasoconstrictory actions, and colonic mobility, as well as antibacterial and antifungal activity.

Serine Carboxypeptidases-

[0024] Carboxypeptidases catalyze the hydrolysis of C-terminal residues of polypeptides. Carboxypeptidases are identified either as metallo-carboxypeptidases or serine-carboxypeptidases.

[0025] Serine carboxypeptidases have the ability to hydrolyze peptides as well as peptide amides from the C-terminus, and have a preferential release of a C-terminal arginine or lysine residue. Their subcellular location is usually extracellular or intracellular. The catalytic activity of serine carboxypeptidases is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which is itself hydrogen bonded to a serine.

Tumor necrosis factors (TNF)-

[0026] Tumor necrosis factors (TNF) alpha and beta are cytokines, which act through TNF receptors to regulate numerous biological processes, including protection against infection and induction of shock and inflammatory disease. The TNF molecules belong to the "TNF-ligand" superfamily, and act together with their receptors or counter-ligands, the "TNF-receptor" superfamily. So far, nine members of the TNF ligand superfamily have been identified and ten members of the TNF-receptor superfamily have been characterized.

[0027] Many members of the TNF-ligand superfamily are expressed by activated T-cells, implying that they are necessary for T-cell interactions with other cell types which underlie cell ontogeny and functions (Meager, A., *supra*).

[0028] Considerable insight into the essential functions of several members of the TNF receptor family has been gained from the identification and creation of mutants that abolish the expression of these proteins. For example, naturally occurring mutations in the FAS antigen and its ligand cause lymphoproliferative disease (Watanabe-Fukunaga, R. *et al., Nature 356*:314 (1992)), perhaps reflecting a failure of programmed cell death. Mutations of the CD40 ligand cause an X-linked immunodeficiency state characterized by high levels of immunoglobulin M and low levels of immunoglobulin G in plasma, indicating faulty T-cell-dependent B-cell activation (Allen, R.C. *et al., Science 259*:990 (1993)). Targeted mutations of the low affinity nerve growth factor receptor cause a disorder characterized by faulty sensory innovation of peripheral structures (Lee, K.F. *et al., Cell 69*:737 (1992)).

[0029] TNF and LT-α are capable of binding to two TNF receptors (the 55- and 75-kd TNF receptors). A large number of biological effects elicited by TNF and LT-α, acting through their receptors, include hemorrhagic necrosis of transplanted tumors, cytotoxicity, a role in endotoxic shock, inflammation, immunoregulation, proliferation and anti-viral responses, as well as protection against the deleterious effects of ionizing radiation. TNF and LT-α are involved in the pathogenesis of a wide range of diseases, including endotoxic shock, cerebral malaria, tumors, autoimmune disease, AIDS and graft-host rejection (Beutler, B. and Von Huffel, C., *Science 264*:667-668 (1994)). Mutations in the p55 Receptor cause increased susceptibility to microbial infection.

[0030] Moreover, an about 80 amino acid domain near the C-terminus of TNFR1 (p55) and Fas was reported as the "death domain," which is responsible for transducing signals for programmed cell death (Tartaglia *et al., Cell 74*:845 (1993)).

[0031] Plasma membrane associated proteins with a predominant tissue expression pattern are important targets for targeted drug delivery, tumor-targeted therapy (e.g., including, but not limited to, radioimmunotherapy) antibody mediated attack of diseased tissues or cancers, and immune mediated cytotoxicity.

[0032] The discovery of new plasma membrane associated proteins and the polynucleotides encoding these molecules thus satisfies a need in the art by not only providing new compositions useful in the diagnosis, treatment, and prevention of diseases associated with cell proliferation and cell signaling, particularly cancer, immune response and neuronal disorders; but also by providing new targets for immune based therapies.

Summary of the Invention

[0033] The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for

identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Detailed Description

Tables

[0034] Table 1 summarizes some of the polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) and contig nucleotide sequence identifier (SEQ ID NO:X)) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby. The first column provides the gene number in the application for each clone identifier. The second column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence disclosed in Table 1. The third column provides a unique contig identifier, "Contig ID:" for each of the contig sequences disclosed in Table 1. The fourth column provides the sequence identifier, "SEQ ID NO:X", for each of the contig sequences disclosed in Table 1. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:X that delineate the preferred open reading frame (ORF) that encodes the amino acid sequence shown in the sequence listing and referenced in Table 1 as SEQ ID NO:Y (column 6). Column 7 lists residues comprising predicted epitopes contained in the polypeptides encoded by each of the preferred ORFs (SEQ ID NO:Y). Identification of potential immunogenic regions was performed according to the method of Jameson and Wolf (CABIOS, 4; 181-186 (1988)); specifically, the Genetics Computer Group (GCG) implementation of this algorithm, embodied in the program PEPTIDESTRUCTURE (Wisconsin Package v10.0, Genetics Computer Group (GCG), Madison, Wisc.). This method returns a measure of the probability that a given residue is found on the surface of the protein. Regions where the antigenic index score is greater than 0.9 over at least 6 amino acids are indicated in Table 1 as "Predicted Epitopes". In particular embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the predicted epitopes described in Table 1. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may

vary slightly. Column 8, "Tissue Distribution" shows the expression profile of tissue, cells, and/or cell line libraries which express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the key provided in Table 4. Expression of these polynucleotides was not observed in the other tissues and/or cell libraries tested. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon), represents the number of times a sequence corresponding to the reference polynucleotide sequence (e.g., SEQ ID NO:X) was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ^{33}P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression. Column 9 provides the chromosomal location of polynucleotides corresponding to SEQ ID NO:X. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Given a presumptive chromosomal location, disease locus association was determined by comparison with the Morbid Map, derived from Online Mendelian Inheritance in Man (Online Mendelian

Inheritance in Man, OMIM™. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, MD) 2000. World Wide Web URL: http://www.ncbi.nlm.nih.gov/omim/). If the putative chromosomal location of the Query overlaps with the chromosomal location of a Morbid Map entry, an OMIM identification number is disclosed in column 10 labeled "OMIM Disease Reference(s)". A key to the OMIM reference identification numbers is provided in Table 5. Column 11 provides the amino acid position of the ALOM hit(s) predicted for the amino acid sequence shown in SEQ ID NO:Y.

[0035] Table 2 summarizes homology and features of some of the polypeptides of the invention. The first column provides a unique clone identifier, "Clone ID NO:Z", corresponding to a cDNA clone disclosed in Table 1. The second column provides the unique contig identifier, "Contig ID:" corresponding to contigs in Table 1 and allowing for correlation with the information in Table 1. The third column provides the sequence identifier, "SEQ ID NO:X", for the contig polynucleotide sequence. The fourth column provides the analysis method by which the homology/identity disclosed in the Table was determined. Comparisons were made between polypeptides encoded by the polynucleotides of the invention and either a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM") as further described below. The fifth column provides a description of the PFAM/NR hit having a significant match to a polypeptide of the invention. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, "Score/Percent Identity", provides a quality score or the percent identity, of the hit disclosed in columns five and six. Columns 8 and 9, "NT From" and "NT To" respectively, delineate the polynucleotides in "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth and sixth columns. In specific embodiments polypeptides of the invention comprise, or alternatively consist of, an amino acid sequence encoded by a polynucleotide in SEQ ID NO:X as delineated in columns 8 and 9, or fragments or variants thereof.

[0036] Table 3 provides polynucleotide sequences that may be disclaimed according to certain embodiments of the invention. The first column provides a unique clone identifier, "Clone ID", for a cDNA clone related to contig sequences disclosed in Table 1. The

second column provides the sequence identifier, "SEQ ID NO:X", for contig sequences disclosed in Table 1. The third column provides the unique contig identifier, "Contig ID:", for contigs disclosed in Table 1. The fourth column provides a unique integer 'a' where 'a' is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, and the fifth column provides a unique integer 'b' where 'b' is any integer between 15 and the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. For each of the polynucleotides shown as SEQ ID NO:X, the uniquely defined integers can be substituted into the general formula of a-b, and used to describe polynucleotides which may be preferably excluded from the invention. In certain embodiments, preferably excluded from the invention are at least one, two, three, four, five, ten, or more of the polynucleotide sequence(s) having the accession number(s) disclosed in the sixth column of this Table. In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table.

[0037] Table 4 provides a key to the tissue/cell source identifier code disclosed in Table 1, column 8. Column 1 provides the tissue/cell source identifier code disclosed in Table 1, Column 8. Columns 2-5 provide a description of the tissue or cell source. Codes corresponding to diseased tissues are indicated in column 6 with the word "disease". The use of the word "disease" in column 6 is non-limiting. The tissue or cell source may be specific (e.g. a neoplasm), or may be disease-associated (e.g., a tissue sample from a normal portion of a diseased organ). Furthermore, tissues and/or cells lacking the "disease" designation may still be derived from sources directly or indirectly involved in a disease state or disorder, and therefore may have a further utility in that disease state or disorder. In numerous cases where the tissue/cell source is a library, column 7 identifies the vector used to generate the library.

[0038] Table 5 provides a key to the OMIM reference identification numbers disclosed in Table 1, column 10. OMIM reference identification numbers (Column 1) were derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of

Medicine, (Bethesda, MD) 2000. World Wide Web URL: http://www.ncbi.nlm.nih.gov/omim/). Column 2 provides diseases associated with the cytologic band disclosed in Table 1, column 9, as determined using the Morbid Map database.

[0039]

Definitions

[0040] The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

[0041] In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

[0042] As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence encoding SEQ ID NO:Y or a fragment or variant thereof; a nucleic acid sequence contained in SEQ ID NO:X (as described in column 3 of Table 1) or the complement thereof; a cDNA sequence contained in Clone ID NO:Z (as described in column 2 of Table 1 and contained within the ATCC Deposit). For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a

polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

[0043] In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown, for example, in column 2 of Table 1, each clone is identified by a cDNA Clone ID (identifier generally referred to herein as Clone ID NO:Z). Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. Furthermore, clones disclosed in this application have been deposited with the ATCC on March 24, 2000, having the ATCC designation numbers PTA-1559. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

[0044] In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

[0045] A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), the polynucleotide sequence delineated in columns 8 and 9 of Table 2 or the complement thereof, and/or cDNA sequences contained in Clone ID NO:Z (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments, or the cDNA clone within the pool of

cDNA clones deposited with the ATCC, described herein). "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 μg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

[0046] Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH_2PO_4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

[0047] Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

[0048] Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

[0049] The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and

double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

[0050] The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA

mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth. Enzymol. 182:626-646 (1990); Rattan et al., Ann. N.Y. Acad. Sci. 663:48-62 (1992)).

[0051] "SEQ ID NO:X" refers to a polynucleotide sequence described, for example, in Tables 1 or 2, while "SEQ ID NO:Y" refers to a polypeptide sequence described in column 6 of Table 1. SEQ ID NO:X is identified by an integer specified in column 4 of Table 1. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. "Clone ID NO:Z" refers to a cDNA clone described in column 2 of Table 1.

[0052] "A polypeptide having functional activity" refers to a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

[0053] The polypeptides of the invention can be assayed for functional activity (e.g. biological activity) using or routinely modifying assays known in the art, as well as assays described herein. Specifically, one of skill in the art may routinely assay polypeptides (including fragments and variants) of the invention for activity using assays as described in the Examples.

[0054] "A polypeptide having biological activity" refers to a polypeptide exhibiting activity similar to, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not

more than about three-fold less activity relative to the polypeptide of the present invention).

[0055] Table 1 summarizes some of the polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and clones (Clone ID NO:Z) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby.

Polynucleotides and Polypeptides of the Invention

It has been discovered herein that the polynucleotides described in Table 1 are predicted to be localized to the plasma membrane of human cells. Accordingly, such polynucleotides, polypeptides encoded by such polynucleotides, and antibodies specific for such polypeptides find use in the diagnosis, treatment, and prevention of diseases associated with cell proliferation and cell signaling, particularly cancer, immune response and neuronal disorders.

Plasma membrane localization was predicted using the following method. All novel contigs in the HGS database were scored using the ALOM program developed by Klein et al. to detect potential transmembrane segments (Klein, P. et al. Biochim. Biophys. Acta 815:468 (1985); which is hereby incorporated by reference in its entirety herein). ALOM attempts to identify the most probable transmembrane segment from the average hydrophobicity value of 17-residue segments, if any. It predicts whether the segment is a transmembrane segment (INTEGRAL) or not (PERIPHERAL) comparing the discriminant score (reported as 'value') with a threshold parameter pre- defined to 0.0 for bacteria ('threshold'). For an integral membrane protein, position(s) of transmembrane segment(s) are also reported. Their length is fixed to 17 but their extension, i.e., the maximal range that satisfies the discriminant criterion, is also given in parentheses. The discrimination step mentioned above is continued after leaving out the segment till there remains no predicted transmembrane segment. The item 'count' is the number of predicted transmembrane segments.

The protein sequence used was the longest start-codon to stop-codon (or end of sequence) ORF. If the ORF was at least 100 amino acids long, and there was a predicted INTEGRAL membrane domain starting at least 40 amino acids downstream of the start

Met, the contig was selected as encoding a plasma-membrane-associated protein. The polynucleotides of the invention are predicted to be plasma membrane associated and comprise the predicted INTEGRAL membrane domains for each unique contig ID shown in column 11 of Table 1.

TABLE 1

Gene No:	Clone ID NO: Z	Contig ID:	SEQ ID NO: X	ORF (From-To)	AA SEQ ID NO: Y	Predicted Epitopes	Tissue Distribution Library code: count (see Table IV for Library Codes)	Cytologic Band	OMIM Disease Reference(s):	ALOM Results
1	HCFNH88	413036	11	64 - 471	1416	Arg-23 to Leu-33, Thr-61 to Phe-73.	AR039: 9, AR033: 5, AR053: 5, AR089: 4, AR096: 4, AR104: 4, AR055: 4, AR060: 4, AR052: 3, AR061: 3 L0619: 1, H0059: 1 and H0423: 1.			44-60
2	HODDW37	456287	12	144 - 572	1417		AR055: 15, AR060: 9, AR052: 7, AR061: 7, AR089: 6, AR033: 6, AR053: 5, AR096: 3, AR104: 1, AR039: 0 L0748: 2, H0328: 1 and H0529: 1.			104-120, 83-99
3	HPMFI38	463734	13	81 - 530	1418		AR060: 6, AR055: 3, AR053: 3, AR096: 2, AR089: 2, AR061: 2, AR033: 2, AR052: 1, AR039: 1, AR104: 1 H0031: 1			80-104, 20-37, 56-72, 134-150
4	HLTDP38	465120	14	171 - 530	1419		AR055: 9, AR060: 6, AR096: 5, AR089: 5, AR033: 4, AR052: 4,			40-57

5	HMHBT30	465711	15	15 - 365	1420	Gln-20 to Ala-26, Ser-53 to Glu-60.	AR061: 4, AR053: 3, AR039: 2, AR104: 1 L0662: 3, L0803: 2, L0805: 2, T0002: 1, H0090: 1, H0412: 1, L0794: 1, L0804: 1, L0655: 1, L0647: 1, L0666: 1 and L0663: 1.				90-113, 59-78, 2-18, 28-44
6	HFCBA57	466000	16	164 - 595	1421		AR033: 8, AR055: 5, AR053: 3, AR089: 3, AR052: 3, AR061: 3, AR039: 3, AR060: 3, AR104: 2, AR096: 2 L0756: 4, L0439: 2, S0412: 2, S0222: 1, H0327: 1, H0009: 1, L0157: 1 and S0031: 1.				31-57, 63-85, 4-23
7	HSRAL33	488966	17	67 - 723	1422	Met-1 to Phe-6, Ser-12 to Asp-17, Ser-100 to Ser-105, Arg-163 to Asp-176, Val-192 to Glu-199.	AR089: 7, AR096: 6, AR053: 5, AR060: 5, AR052: 4, AR039: 4, AR104: 4, AR055: 4, AR033: 3, AR061: 1	7q31		126650, 126650, 164860, 180105, 222800,	126-143

						L0777: 4, L0766: 3, H0014: 2, L0731: 2, L0758: 2, S0282: 1, S0007: 1, S0280: 1, H0575: 1, H0328: 1, L0369: 1, L0637: 1, L0771: 1, L0768: 1, L0803: 1, L0655: 1, L0809: 1, S0380: 1, H0521: 1, H0627: 1, S3014: 1, L0748: 1, L0608: 1, S0011: 1 and S0192: 1.	246900, 274600, 274600, 602081	89-105	
8	HSSMQ84	502907	18	20 - 415	1423	Pro-52 to Pro-57.	AR055: 8, AR052: 5, AR033: 4, AR061: 4, AR060: 4, AR089: 3, AR096: 3, AR039: 3, AR104: 3, AR053: 3 L0596: 2, L0588: 2, H0135: 1, H0056: 1, L0369: 1, L0803: 1, H0520: 1, S0027: 1 and S0276: 1.			
9	HUKAB82	503441	19	74 - 424	1424	Leu-9 to Arg-18, Phe-109 to Gly-115.	AR060: 140, AR055: 117, AR104: 113, AR039: 111, AR061: 92, AR033: 72, AR053: 70, AR052: 66, AR089: 55, AR096: 21 L0748: 5, L0749: 5, L0439: 3, L0779: 2, L0731: 2, H0556: 1, S0356: 1, H0575: 1, H0597: 1, H0551:		72-90	

							1, H0413: 1, H0059: 1, L0770: 1, L0771: 1, L0655: 1, H0144: 1, S0378: 1, L0747: 1 and S0276: 1.			52-68
10	HDPPP46	506828	20	29 - 328	1425		AR096: 4, AR033: 3, AR039: 3, AR089: 3, AR055: 3, AR052: 2, AR061: 2, AR053: 1, AR060: 1, AR104: 1 L0766: 4, H0617: 2, L0662: 2, H0690: 2, H0295: 1, H0662: 1, S0354: 1, H0729: 1, H0318: 1, H0545: 1, H0266: 1, H0401: 1, H0135: 1, H0087: 1, L5575: 1, L0803: 1, L0523: 1, L0383: 1, L0665: 1, H0703: 1, H0539: 1, H0521: 1, H0522: 1, S0406: 1, S0028: 1, L0779: 1 and H0352: 1.			
11	HMTME11	506893	21	72 - 425	1426	Met-1 to Arg-11, Gly-30 to Arg-39.	AR052: 5, AR053: 5, AR096: 4, AR055: 4, AR089: 4, AR033: 3, AR060: 3, AR039: 2, AR104: 2, AR061: 2 L0775: 3, H0624: 2, L0471: 2, S0051: 2, L0768: 2, H0659: 2, L0759: 2, L0605: 2, S0192: 2, S0114:			100-118

								9-41, 83-106, 54-76
						1, S0116: 1, H0638: 1, H0125: 1, H0489: 1, S0222: 1, L0623: 1, T0115: 1, H0327: 1, H0687: 1, T0023: 1, H0031: 1, H0673: 1, L0065: 1, L0520: 1, L0769: 1, L0653: 1, L0783: 1, L0809: 1, L0519: 1, L0543: 1, H0658: 1, H0670: 1, H0672: 1, S0330: 1, S0378: 1, S0380: 1, H0525: 1, H0436: 1, S3012: 1, L0777: 1, L0731: 1, H0653: 1, H0543: 1, H0422: 1 and H0352: 1.		
							AR055: 11, AR060: 8, AR033: 5, AR061: 5, AR052: 5, AR089: 4, AR104: 4, AR096: 4, AR039: 4, AR053: 4 L0439: 4, L0803: 3, H0590: 2, L0483: 2, H0163: 2, L0805: 2, S0374: 2, H0658: 2, H0696: 2, H0717: 1, S0116: 1, S0358: 1, L0717: 1, H0052: 1, H0194: 1, H0184: 1, L0738: 1, H0545: 1, S0316: 1, S0003: 1, S0364: 1, S0366: 1, S0036: 1, H0272: 1, L0638:	
					1427			
				12 - 386				
			22					
		507310						
	HBMUK46							
12								

							1, L0766: 1, L0776: 1, L0789: 1, L0664: 1, L0665: 1, H0710: 1, H0521: 1, S0013: 1, S0406: 1, L0744: 1, L0752: 1, L0758: 1, L0605: 1, S0026: 1 and H0543: 1.			138-154, 8-24
13	HETDT70	509728	23		1428		AR052: 319, AR096: 250, AR089: 171, AR060: 143, AR053: 121, AR104: 71, AR039: 57, AR033: 51, AR061: 51, AR055: 14 L0752: 3, L0748: 2, L0740: 2, L0731: 2, S0358: 1, H0438: 1, H0574: 1, H0046: 1, H0041: 1, H0272: 1, S0150: 1, L0794: 1, L0803: 1, L0804: 1, L0775: 1, L0661: 1, L0789: 1, H0672: 1, H0539: 1, L0758: 1 and S0436: 1.			
14	HPWBL19	521848	24	60 - 362	1429	Pro-15 to Ser-21, Ser-60 to Tyr-65, Glu-90 to Asp-101.	AR033: 1, AR089: 1, AR053: 1, AR104: 1, AR061: 1, AR096: 0, AR055: 0, AR060: 0, AR052: 0 L0766: 6, L0740: 5, H0135: 1, L0769: 1, L0383: 1, S0044: 1, L0750: 1 and			62-89, 25-46

15	HMKAD85	523186	25	48 - 422	1430			L0752: 1.				88-104, 49-65
								AR033: 2, AR053: 2, AR089: 1, AR104: 1, AR061: 1, AR055: 1, AR060: 1, AR096: 0, AR039: 0, AR052: 0 S0007: 2, H0392: 2, L0745: 1, L0753: 1, L0759: 1 and L0589: 1.				
16	HE9NE12	524559	26	68 - 598	1431	Lys-12 to Lys-17, Thr-39 to Lys-45, Thr-49 to Glu-57, Thr-59 to Glu-69, Glu-80 to Ile-90, Gly-122 to Met-127, Lys-170 to Asn-177.		AR104: 1, AR096: 1, AR033: 1, AR089: 1, AR060: 1, AR061: 1, AR052: 0, AR055: 0, AR053: 0, AR039: 0 L0766: 5, L0438: 4, L0439: 4, L0803: 3, L0759: 3, H0445: 3, H0046: 2, L0157: 2, L0762: 2, L0363: 2, L0794: 2, L0774: 2, L0776: 2, L0790: 2, L0666: 2, H0144: 2, L0748: 2, L0749: 2, H0556: 1, H0159: 1, H0716: 1, H0459: 1, S0418: 1, L0005: 1, H0580: 1, S0046: 1, H0612: 1, H0586: 1, H0050: 1, L0471: 1, H0615: 1, H0488: 1, S0426: 1, H0529: 1, L0520: 1, L0638: 1, L0667: 1,				96-113

							L0373: 1, L0378: 1, L0805: 1, L0659: 1, L0526: 1, L0809: 1, L0663: 1, S0374: 1, H0711: 1, H0670: 1, H0521: 1, L0777: 1, L0780: 1, L0485: 1, L0097: 1, S0192: 1, H0543: 1, H0423: 1 and H0506: 1.	8p23	148370	81-102, 22-38
17	HE2AX73	525950	27	12 - 317	1432	Leu-15 to Ser-21.	AR053: 4, AR061: 4, AR052: 3, AR055: 3, AR039: 3, AR060: 3, AR089: 2, AR096: 2, AR033: 1, AR104: 1 H0170: 2			
18	HHGBV89	527491	28	53 - 376	1433	Arg-56 to Phe-61.	AR055: 16, AR061: 7, AR052: 7, AR060: 6, AR033: 5, AR089: 5, AR053: 5, AR096: 3, AR039: 0, AR104: 0 H0052: 5, L0748: 5, L0756: 4, L0731: 4, S0360: 3, L0764: 3, L0747: 3, L0749: 3, H0255: 2, H0333: 2, L0055: 2, L0653: 2, L0740: 2, L0754: 2, L0750: 2, L0596: 2, H0352: 2, H0556: 1, H0341: 1, H0662: 1, H0306: 1, H0402: 1, H0036: 1, H0434: 1, H0150:			64-80, 15-31

							1, H0252: 1, L0456: 1, H0135: 1, H0413: 1, H0059: 1, H0529: 1, L0770: 1, L0769: 1, L0630: 1, L0521: 1, L0662: 1, L0775: 1, L0776: 1, L0493: 1, H0684: 1, S0328: 1, S0044: 1, L0777: 1, L0752: 1, L0755: 1, L0758: 1 and S0242: 1.			48-65
19	HTTDC06	529791	29	1 - 405	1434	Lys-13 to Asp-24, Pro-32 to Arg-40.	AR039: 14, AR055: 14, AR033: 11, AR053: 11, AR052: 11, AR060: 10, AR104: 10, AR096: 9, AR089: 8, AR061: 8 S0380: 2, L0742: 2, L0779: 2, L0759: 2, H0333: 1, H0039: 1, H0040: 1, H0625: 1, H0561: 1, L0666: 1, L0663: 1, H0672: 1, L0747: 1, L0777: 1, L0758: 1 and H0444: 1.			
20	HFXKR35	532045	30	531 - 16	1435	Asn-54 to Gly-60, Pro-166 to Pro-171.	AR089: 1, AR061: 1, AR053: 1, AR096: 1, AR060: 1, AR104: 1, AR033: 0, AR055: 0, AR039: 0, AR052: 0 L0777: 5, S0436: 5, S0116: 3, L0805: 3, L0809: 3, H0696: 3, H0423: 3, S0282:			125-157, 4-29, 67-86, 36-52, 106-122

										56-73
21	HHSDL85	534414	31	17 - 373	1436		Ser-7 to Gln-20, Pro-24 to Phe-34, Gly-76 to Gly-84.	2, S0354: 2, H0083: 2, H0316: 2, L0763: 2, L0767: 2, L0776: 2, S0406: 2, L0779: 2, S0114: 1, H0657: 1, H0656: 1, S0358: 1, S0444: 1, S0360: 1, H0340: 1, S0046: 1, H0619: 1, H0455: 1, H0333: 1, H0574: 1, H0559: 1, T0109: 1, H0156: 1, L0021: 1, T0074: 1, H0618: 1, H0318: 1, S0474: 1, S0049: 1, H0327: 1, H0530: 1, H0615: 1, H0553: 1, H0673: 1, H0708: 1, H0059: 1, L0065: 1, S0438: 1, H0207: 1, S0422: 1, L0520: 1, L0769: 1, L0761: 1, L0521: 1, L0774: 1, L0655: 1, L0659: 1, L0526: 1, L0793: 1, L0666: 1, L0664: 1, H0659: 1, H0518: 1, S0268: 1, S0176: 1, H0478: 1, S0390: 1, L0748: 1, L0750: 1, L0755: 1, L0731: 1, L0608: 1, L0362: 1, S0026: 1 and S0242: 1.	AR055: 4, AR039: 3, AR060: 2, AR033: 2, AR053: 2, AR061: 2,

							AR104: 2, AR089: 2, AR096: 2, AR052: 2 S0007: 3, S0001: 1, H0618: 1, H0009: 1, S0051: 1, L0763: 1, L0439: 1 and L0758: 1.			
22	HTECA32	535036	32	88 - 438	1437	Pro-15 to Thr-24, Glu-39 to Trp-47.	AR033: 54, AR055: 51, AR061: 43, AR089: 40, AR053: 38, AR060: 38, AR052: 26, AR096: 11, AR104: 10, AR039: 5 H0038: 2			49-65
23	HTEHL79	535040	33	37 - 453	1438	Arg-14 to Asp-20.	AR033: 112, AR052: 80, AR096: 68, AR053: 67, AR089: 65, AR104: 61, AR060: 58, AR061: 55, AR039: 52, AR055: 38 H0052: 2, H0616: 2, L0779: 2, L0777: 2, H0656: 1, H0549: 1, H0038: 1, L0748: 1, L0758: 1, L0601: 1 and H0543: 1.			49-65
24	HPJBL54	536712	34	156 - 488	1439		AR055: 17, AR053: 9, AR060: 9, AR033: 9, AR061: 8, AR039: 7, AR089: 6, AR052: 6, AR104: 6, AR096: 5 S0418: 3, L0439: 3, L0595: 2, H0542: 2, H0656:	15q15.1	114240, 224120, 600839, 602099	46-62, 26-42

						1, H0638: 1, S0420: 1, S0045: 1, H0253: 1, H0267: 1, H0553: 1, S0150: 1, L0438: 1, H0519: 1, S0126: 1, H0660: 1, S0152: 1 and H0543: 1.				81-98, 13-29, 175-191, 62-78
25	HSDDD20	538217	35	64 - 753	1440	Asp-46 to Glu-59.	AR096: 1, AR055: 1, AR089: 1, AR060: 1, AR039: 1, AR033: 0, AR061: 0, AR053: 0, AR052: 0, AR104: 0 S0028: 3, S0001: 2, H0617: 2, L0361: 2, S0356: 1, S0045: 1, H0619: 1, S0278: 1, H0250: 1, H0231: 1, H0181: 1, S0390: 1 and S0031: 1.			
26	HCUCG74	550208	36	588-929	1441		AR052: 3, AR096: 2, AR053: 2, AR033: 2, AR089: 2, AR061: 2, AR060: 1, AR055: 1, AR104: 1, AR039: 0 L0789: 4, H0306: 2, L0809: 2, L0759: 2, L0596: 2, H0402: 1, H0580: 1, H0550: 1, H0370: 1, H0404: 1, H0559: 1, H0486: 1, H0031: 1, H0674: 1, H0135: 1, H0100: 1, L0800: 1,			177-193, 149-165

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27	HFIXK94	550992	37	96 - 404	1442		AR033: 4, AR089: 3, AR060: 2, AR055: 2, AR052: 1, AR053: 1, AR061: 1, AR096: 0, AR039: 0, AR104: 0 S0242: 1 and S0196: 1.			
28	HPJAV46	551777	38	24 - 362	1443	Pro-69 to Gln-77.	AR089: 45, AR096: 43, AR060: 39, AR039: 37, AR055: 27, AR104: 20, AR033: 20, AR052: 19, AR053: 14, AR061: 14 H0250: 60, S0126: 24, H0013: 9, H0124: 9, H0494: 8, H0521: 7, H0428: 6, H0553: 6, H0644: 6, H0038: 6, S0027: 6, S0040: 5, T0039: 5, H0050: 5, L0471: 5, H0135: 5, H0551: 5, T0067: 5, H0144: 5, H0539: 5, S0028: 5, L0439: 5, L0740: 5, H0171: 4, S0356: 4, S0046: 4, H0586: 4, H0486: 4, H0599: 4, H0046: 4, H0024: 4, H0266: 4, S0003: 4, H0040: 4, H0059:			7-37, 89-113, 45-62

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29	HTTDL61	558312	39	21 - 329	1444		AR053: 16, AR096: 14, AR052: 14, AR055: 13, AR089: 11, AR060: 9, AR033: 9, AR104: 6, AR061: 5, AR039: 3 H0038: 8, H0616: 4, L0779: 3, L0758: 3, L0753: 2, L0032: 1, T0006: 1, H0040: 1, S0002: 1, L0768: 1, S0053: 1 and H0547: 1.			42-67, 3-19
30	HFPBN94	561612	40	1235 - 885	1445	Ser-60 to Ser-66.	AR039: 13, AR053: 11, AR055: 9, AR089: 9, AR033: 9, AR060: 7, AR096: 7, AR052: 7, AR061: 5, AR104: 5 S0222: 1			36-61, 92-110
31	HYBBG69	562024	41	401 - 1144	1446	Arg-35 to Cys-46, Phe-52 to Met-57, Thr-70 to Gly-84, Thr-88 to Glu-109, Gly-151 to Gly-159, Ser-167 to Thr-175, Ala-193 to Phe-206, Arg-215 to Gly-223.	AR052: 4, AR061: 3, AR055: 3, AR053: 3, AR089: 2, AR033: 2, AR060: 2, AR039: 1, AR096: 1, AR104: 1 S0002: 70, S0426: 29, S0278: 28, S0003: 28, H0521: 28, S0344: 27, S0142: 14, L0747: 14, H0090: 13, S0144: 13,			1-33, 230-247, 125-141

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32	HDPOJ05	562077	42	350 -	1447	Met-1 to Gly-6,	1, H0638: 1, S0358: 1, S0376: 1, T0008: 1, S0132: 1, H0619: 1, H0645: 1, H0351: 1, H0411: 1, L0623: 1, H0427: 1, S0280: 1, L0022: 1, T0082: 1, H0036: 1, H0390: 1, L0105: 1, H0544: 1, H0041: 1, H0009: 1, H0620: 1, H0015: 1, H0373: 1, S6028: 1, H0039: 1, H0031: 1, H0644: 1, L0142: 1, L0143: 1, H0673: 1, H0674: 1, S0364: 1, H0316: 1, T0067: 1, H0100: 1, H0494: 1, S0370: 1, S0466: 1, H0509: 1, L0763: 1, L0769: 1, L0638: 1, L0373: 1, L0764: 1, L0561: 1, L0803: 1, L0774: 1, L0375: 1, L0806: 1, L0653: 1, L0776: 1, L0655: 1, L0607: 1, L0657: 1, L0782: 1, L0529: 1, L0790: 1, L0664: 1, H0144: 1, H0684: 1, H0435: 1, H0672: 1, S0330: 1, H0555: 1, S3012: 1, L0748: 1, L0757: 1, H0595: 1, L0584: 1, L0597: 1 and H0352: 1.	AR096: 1, AR089: 1,		35-62

			664		Pro-23 to Asp-37.	AR061: 0, AR055: 0, AR033: 0, AR104: 0, AR053: 0, AR052: 0, AR060: 0 H0250: 5, L0740: 4, - H0657: 3, L0761: 3, L0659: 3, L0809: 3, L0717: 2, H0620: 2, H0135: 2, H0063: 2, H0100: 2, L0789: 2, L0751: 2, L0750: 2, L0731: 2, H0543: 2, S0116: 1, H0255: 1, H0664: 1, H0580: 1, H0253: 1, H0581: 1, H0421: 1, H0123: 1, H0179: 1, H0617: 1, H0606: 1, H0163: 1, L0638: 1, L0771: 1, L0794: 1, L0766: 1, L0650: 1, L0655: 1, L0783: 1, L0532: 1, L0666: 1, H0520: 1, H0547: 1, H0660: 1, H0648: 1, S0380: 1, H0521: 1, H0522: 1, H0555: 1, L0756: 1, L0779: 1, S0436: 1 and S0276: 1.			42-66, 67-84, 9-25
33	HMAGF64	562775	43	39 - 428	1448	Leu-30 to Thr-35, Phe-38 to Gly-44.	AR052: 7, AR053: 4, AR089: 3, AR060: 3, AR096: 3, AR033: 2, AR061: 2, AR039: 2, AR055: 2, AR104: 2 S0278: 1 and H0445: 1.			

34	HACCO38	563589	44	143 - 700	1449	Lys-14 to Asp-24, Gln-114 to Leu-119, Asp-122 to Arg-127.	AR053: 12, AR052: 11, AR089: 8, AR096: 8, AR055: 7, AR060: 7, AR033: 5, AR061: 5, AR104: 4, AR039: 3 T0023: 2, L0662: 2, S0330: 2, L0749: 2, L0758: 2, S0356: 1, S0358: 1, S0360: 1, S0408: 1, L0586: 1, S0280: 1, H0590: 1, H0581: 1, H0052: 1, H0014: 1, S0003: 1, H0316: 1, H0591: 1, S0450: 1, S0150: 1, S0426: 1, L0766: 1, S0216: 1, L0747: 1, L0756: 1, L0752: 1 and L0596: 1.			138-155, 83-99, 35-51, 59-75
35	HRAAM31	567314	45	14 - 355	1450	Met-1 to Gly-6.	AR039: 35, AR053: 29, AR104: 28, AR033: 25, AR052: 23, AR096: 22, AR055: 19, AR089: 18, AR060: 13, AR061: 10 H0555: 1			23-40, 50-66
36	HWDAA03	571474	46	296 - 670	1451		AR096: 2, AR089: 1, AR039: 1, AR052: 1, AR033: 1, AR104: 1, AR060: 0, AR061: 0, AR055: 0 H0600: 1 and S0002: 1.			71-87, 98-114
37	HTHCV60	572607	47	93 - 473	1452		AR096: 14, AR089: 12,			73-89,

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38	HTLEV17	573110	48	15 - 428	1453		AR039: 14, AR033: 10, AR053: 9, AR055: 7, AR104: 7, AR089: 7, AR096: 6, AR052: 5, AR060: 5, AR061: 4 L0741: 3, L0438: 2, S0222: 1, H0427: 1, H0618: 1, H0253: 1, H0284: 1, S0038: 1, H0494: 1, S0144: 1, L0743: 1 and L0366: 1.			84-101
39	HCFAB91	573179	49	70 - 438	1454	Lys-22 to Gly-28, Lys-39 to Glu-48, Ser-54 to Trp-59.	AR089: 4, AR096: 3, AR033: 3, AR052: 3, AR060: 2, AR055: 2, AR053: 1, AR061: 1, AR104: 1, AR039: 0 H0422: 2, H0339: 1 and L0769: 1.			68-88
40	HMWEE18	573751	50	356 - 700	1455	His-13 to Ser-21.	AR055: 11, AR060: 7, AR052: 5, AR089: 5, AR061: 5, AR033: 5, AR053: 5, AR096: 4, AR039: 4, AR104: 3 L0747: 3, L0754: 2,			81-115

								L0599: 2, H0713: 1, H0341: 1, S0360: 1, H0601: 1, H0592: 1, H0123: 1, H0494: 1, H0660: 1, L0756: 1 and L0779: 1.			46-62
41	HTLAI85	574924	51	46 - 354	1456			AR053: 16, AR052: 14, AR096: 12, AR089: 10, AR104: 7, AR060: 6, AR055: 6, AR033: 5, AR061: 3, AR039: 3 H0617: 7, L0438: 6, L0439: 5, H0253: 4, L0794: 3, L0766: 3, L0791: 3, H0618: 2, S0344: 2, L0769: 2, L0662: 2, L0758: 2, H0556: 1, H0733: 1, H0333: 1, T0040: 1, H0013: 1, H0575: 1, H0318: 1, H0052: 1, H0178: 1, H0023: 1, H0083: 1, T0023: 1, H0606: 1, H0135: 1, T0004: 1, H0509: 1, S0144: 1, L0803: 1, L4501: 1, L0663: 1, L0665: 1, H0672: 1, H0631: 1, L0744: 1, L0747: 1, L0756: 1, L0779: 1, L0731: 1, S0436: 1, S0194: 1 and H0542: 1.			
42	HHPGQ38	575287	52	225 -	1457	Leu-3 to Gln-18.		AR055: 14, AR060: 13,			61-79

				530						
43	HNGER82	576739	53	229 - 639	1458	Gln-22 to Gly-28, Thr-109 to Gly-114, Phe-117 to Arg-124.	AR089: 12, AR096: 10, AR052: 8, AR033: 8, AR061: 7, AR053: 5, AR104: 0, AR039: 0 L0756: 2, H0051: 1, S0380: 1, L0748: 1 and L0753: 1.			68-86, 89-108, 40-56
44	HBJLU13	578925	54	252 - 551	1459	Gly-35 to Gln-41, Phe-51 to Lys-57.	AR060: 10, AR089: 8, AR033: 7, AR104: 2, AR061: 1, AR053: 1, AR096: 1, AR055: 1, AR039: 0 H0123: 2 and H0318: 1.			63-84
45	HCFDC55	581501	55	73 - 426	1460		AR033: 5, AR052: 4, AR089: 4, AR053: 4, AR055: 3, AR060: 2, AR096: 2, AR061: 2, AR039: 1 L0438: 4, L0803: 3, H0169: 2, L0526: 2, H0657: 1, S0408: 1, H0421: 1,			53-75, 92-112, 25-45

							H0050: 1, S0370: 1, L0637: 1, L0646: 1, L0800: 1, L0662: 1, L0766: 1, L0607: 1, L0659: 1, L0665: 1, L0352: 1, H0659: 1, H0651: 1, S0328: 1, H0436: 1, L0777: 1, L0752: 1, S0242: 1 and H0422: 1.			
46	HFKCT25	586810	56	178 - 591	1461	Leu-12 to Gly-18, Tyr-27 to Glu-34, Lys-127 to Pro-132.	AR053: 2, AR089: 2, AR060: 2, AR096: 1, AR055: 1, AR061: 1, AR033: 1, AR104: 1, AR039: 0, AR052: 0 H0012: 3, L0794: 3, L0766: 2, L0788: 2, S0192: 2, H0618: 1, H0015: 1, H0073: 1, T0023: 1, H0063: 1, L0763: 1, L0787: 1, L0532: 1, S3012: 1, S0027: 1, L0747: 1, L0750: 1, L0731: 1 and S0276: 1.			83-101, 62-78
47	HAPOW05	587520	57	13 - 330	1462	Lys-2 to Ser-10, Gln-20 to Leu-25, Val-29 to Arg-53.	AR055: 15, AR039: 15, AR033: 13, AR104: 12, AR061: 12, AR053: 10, AR089: 9, AR060: 9, AR052: 8, AR096: 8 L0748: 2 and H0575: 1.			66-82
48	HCUFP05	589293	58	660 - 331	1463	Gly-2 to Leu-7, Pro-11 to Leu-26,	AR033: 4, AR089: 3, AR096: 2, AR061: 2,	11q13	102200, 106100,	57-86

						Gly-28 to Ala-40, Arg-51 to Pro-58, Asp-92 to Leu-97.	AR060: 2, AR055: 2, AR104: 1, AR039: 0, AR052: 0, AR053: 0 L0769: 9, L0752: 6, L0747: 5, L0759: 5, L0764: 4, L0806: 4, L0758: 4, H0549: 3, L0770: 3, L0783: 3, L0750: 3, S0408: 2, H0687: 2, L0771: 2, L0662: 2, L0794: 2, L0775: 2, L0805: 2, L0776: 2, L0809: 2, L0666: 2, L0756: 2, L0779: 2, L0757: 2, H0294: 1, S0134: 1, H0664: 1, H0402: 1, H0586: 1, H0486: 1, L0021: 1, H0081: 1, H0012: 1, H0014: 1, H0688: 1, T0006: 1, L0763: 1, L5565: 1, L0761: 1, L0772: 1, L0800: 1, L0773: 1, L0767: 1, L0768: 1, L0766: 1, L0803: 1, L0774: 1, L0659: 1, L0788: 1, L0792: 1, H0520: 1, H0670: 1, L0786: 1, L0777: 1 and L0731: 1.		131100, 131100, 131100, 133780, 147050, 153700, 161015, 164009, 168461, 168461, 168461, 180721, 180840, 191181, 193235, 209901, 232600, 259700, 259770, 600045, 600319, 600528, 601884	
49	HE8CX53	597069	59	161 - 514	1464	Gln-28 to Pro-41, Lys-94 to Pro-108.	AR096: 16, AR053: 14, AR055: 14, AR052: 11, AR060: 8, AR089: 8, AR033: 8, AR104: 7,	Xq22.3-q23	300046, 300067, 300067, 300121,	56-72, 1-17, 76-92

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50	HCENB31	597213	60	65 - 508	1465		AR104: 19, AR033: 15, AR039: 5, AR061: 5, AR053: 5, AR096: 5, AR052: 4, AR055: 4, AR089: 4, AR060: 3 H0052: 3, S0001: 2, S0222: 1, H0194: 1, L0157: 1, L0369: 1, L0769: 1, L0767: 1, L0794: 1, H0144: 1 and L0438: 1.	9q22.1-q22.3	162400, 227645, 229700, 278700, 601309, 601309, 602014, 602088	42-60, 4-22
51	H7TME55	597832	61	151 - 498	1466	Val-40 to Tyr-45.	AR053: 1, AR055: 1, AR096: 1, AR089: 1, AR061: 0, AR060: 0, AR104: 0, AR033: 0, AR052: 0, AR039: 0 S0184: 26 and S0186: 8.	10q11.2-q21.1	129010, 154545, 164761, 164761, 164761, 164761, 188550, 601386, 601493	47-66, 16-32

52	HDHMA49	600734	62	75 - 539	1467	Ser-15 to His-22, Pro-46 to Pro-52, Gly-63 to Ser-69, Arg-111 to Ser-116, Pro-121 to Asn-129, Ala-136 to Gly-145.	AR060: 18, AR055: 16, AR104: 14, AR061: 14, AR033: 11, AR089: 11, AR039: 7, AR096: 6, AR053: 5, AR052: 4 L0439: 13, L0438: 6, H0052: 3, H0009: 2, L0769: 2, L0794: 2, L0741: 2, H0229: 1, H0572: 1, H0569: 1, L0770: 1, L0796: 1, L5566: 1, L0805: 1, L0789: 1 and L0786: 1.			80-111
53	HBXBG68	610609	63	18 - 362	1468		AR096: 5, AR055: 3, AR039: 2, AR061: 2, AR033: 2, AR089: 2, AR104: 2, AR052: 2, AR060: 1, AR053: 1 S0038: 1			60-77
54	HGBFC53	613240	64	122 - 472	1469	Thr-8 to Glu-13, Thr-89 to Leu-96.	AR033: 10, AR055: 9, AR104: 6, AR052: 5, AR089: 5, AR096: 5, AR060: 5, AR061: 4, AR053: 4, AR039: 2 L0757: 13, L0759: 7, L0747: 6, T0010: 5, L0748: 5, L0770: 4, L0764: 4, L0750: 4, H0031: 3, L0438: 3, L0756: 3, L0758: 3, H0013: 2, S0010: 2, H0135:			100-116, 14-30

							2, L0598: 2, L0761: 2, L0646: 2, L0766: 2, L0775: 2, L0806: 2, L0776: 2, L0657: 2, L0659: 2, L0666: 2, S0328: 2, L0439: 2, L0777: 2, L0731: 2, L0592: 2, L0362: 2, H0265: 1, H0556: 1, H0222: 1, S0418: 1, L0005: 1, S0356: 1, S0358: 1, S0468: 1, H0208: 1, S0046: 1, H0619: 1, S0222: 1, H0370: 1, H0587: 1, H0497: 1, H0331: 1, H0486: 1, T0039: 1, H0156: 1, H0575: 1, T0082: 1, H0706: 1, S0346: 1, H0318: 1, H0581: 1, H0052: 1, H0309: 1, H0545: 1, H0178: 1, H0123: 1, S0050: 1, H0014: 1, H0051: 1, S6028: 1, H0286: 1, H0328: 1, H0032: 1, L0455: 1, H0316: 1, H0164: 1, S0386: 1, L0351: 1, L0435: 1, T0042: 1, H0359: 1, H0646: 1, H0026: 1, L0763: 1, L0796: 1, L0662: 1, L0626: 1, L0767: 1, L0387: 1, L0651: 1, L0655: 1, L0807: 1, L0658: 1, L0558: 1, L0783:			

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55	HPMCK47	613734	65	336 - 767	1470	Thr-91 to Pro-97.	AR055: 8, AR060: 5, AR061: 4, AR089: 4, AR033: 4, AR096: 4, AR039: 3, AR053: 3, AR104: 2, AR052: 2 L0754: 7, H0644: 4, H0031: 2, L0748: 1, L0747: 1 and H0543: 1.			107-139
56	HAPNX53	613777	66	5 - 478	1471	Ala-15 to Glu-26, Lys-33 to Ser-47, Cys-53 to Thr-60, Cys-119 to Trp-127.	AR055: 7, AR061: 6, AR060: 5, AR096: 4, AR033: 4, AR052: 3, AR089: 3, AR053: 3, AR104: 2, AR039: 2 H0575: 4, H0271: 3, H0250: 1 and L0599: 1.			61-97
57	HOFAE02	614169	67	129 - 434	1472	Thr-10 to Ala-20, Asp-82 to Asn-102.	AR033: 7, AR060: 4, AR096: 3, AR089: 3, AR053: 3, AR061: 3, AR052: 2, AR055: 1,			21-42, 44-66

						AR104: 1, AR039: 0 S0136: 7, S0356: 2, S0410: 2, H0486: 2, H0672: 2, H0170: 1, H0657: 1, H0692: 1, H0254: 1, H0402: 1, H0305: 1, S0358: 1, H0619: 1, L0717: 1, H0406: 1, H0415: 1, H0599: 1, S0010: 1, T0115: 1, H0545: 1, S0051: 1, H0617: 1, H0264: 1, H0100: 1, L0659: 1, L0789: 1, L0665: 1, H0519: 1, H0414: 1, S0406: 1, H0422: 1 and H0352: 1.			143-159
58	HSLIQ83	614801	68	16 - 525	1473		AR055: 5, AR033: 5, AR060: 4, AR104: 4, AR053: 4, AR089: 3, AR052: 3, AR061: 3, AR096: 2, AR039: 1 L0439: 6, L0438: 3, L0809: 2, L0748: 2, H0583: 1, S0001: 1, T0010: 1, L0456: 1, H0598: 1, L0761: 1, L0783: 1, S0028: 1, L0749: 1, L0756: 1, S0458: 1 and H0352: 1.			143-159
59	HNTMD04	615231	69	234 - 593	1474	Ser-19 to Val-24, Pro-35 to Asn-42, Pro-44 to Gly-59,	AR039: 6, AR053: 4, AR052: 3, AR033: 3, AR096: 3, AR055: 3,			78-96

						Gly-96 to Gly-101.	AR089: 3, AR060: 2, AR061: 2, AR104: 2 L0755: 3, H0521: 2, L0754: 2, L0747: 2, S0003: 1, L0369: 1, L0667: 1, L0659: 1, L0647: 1, L0790: 1, L0663: 1, L0664: 1, H0520: 1, H0518: 1, S0152: 1, S0404: 1, H0436: 1, L0748: 1 and H0423: 1.			92-111, 45-61
60	HRABY48	616154	70	47 - 379	1475	Thr-17 to Ser-28, Ser-39 to Gly-45.	AR104: 20, AR096: 11, AR089: 8, AR033: 7, AR052: 5, AR060: 5, AR053: 5, AR039: 4, AR055: 2, AR061: 1 H0599: 1, H0555: 1 and S0390: 1.			
61	HDDAA17	616652	71	345 - 680	1476	Arg-5 to Glu-10.	AR055: 12, AR089: 8, AR033: 8, AR061: 7, AR060: 7, AR053: 5, AR052: 5, AR096: 4, AR039: 1, AR104: 0 L0758: 2, H0339: 1, L0664: 1 and L0731: 1.			60-76
62	HTRAC41	618715	72	110 - 748	1477	Glu-121 to Asp-128.	AR096: 1, AR089: 1, AR104: 1, AR033: 0, AR052: 0, AR061: 0, AR039: 0, AR060: 0, AR055: 0, AR053: 0			48-81, 126-156, 89-115, 21-38, 1-17, 180-

							S0001: 2, H0730: 2, L0581: 2, H0713: 1, H0735: 1, H0164: 1 and S0028: 1.			196, 161-177
63	HOSCV06	619875	73	57 - 407	1478	Val-45 to Glu-52, Ala-82 to Ala-93, Pro-103 to Asp-108.	AR039: 25, AR055: 11, AR033: 10, AR053: 10, AR096: 9, AR060: 9, AR052: 9, AR089: 9, AR104: 8, AR061: 6 S0003: 1, L0498: 1 and L0599: 1.			52-68, 26-42
64	HMCHS27	620219	74	1 - 519	1479	Arg-78 to Glu-84, Leu-94 to Trp-102, Lys-113 to Thr-118.	AR055: 10, AR052: 9, AR053: 8, AR033: 7, AR089: 6, AR060: 6, AR096: 4, AR061: 4, AR104: 1, AR039: 0 H0441: 1, H0409: 1 and S0344: 1.			46-64, 130-146
65	HEMFC09	625334	75	221 - 670	1480		AR060: 2, AR039: 1, AR053: 1, AR104: 1, AR033: 1, AR096: 1, AR089: 1, AR061: 1, AR055: 0, AR052: 0 L0755: 3, S0003: 2, H0521: 2, S0470: 1, S0354: 1, S0444: 1, S0360: 1, S0046: 1, H0574: 1, S0010: 1, H0046: 1, L0471: 1, H0051: 1, H0553: 1, H0646: 1, S0210: 1, H0529: 1,			81-99, 34-50

66	HNTRJ16	625432	76	25 - 798	1481	Glu-90 to Asn-95, Arg-101 to Lys-108.	L0662: 1, H0659: 1, H0658: 1, H0539: 1, H0436: 1, L0758: 1, L0599: 1, S0192: 1, S0276: 1 and H0423: 1.			57-73
							AR053: 3, AR052: 3, AR096: 2, AR033: 2, AR055: 2, AR089: 2, AR060: 1, AR061: 1, AR104: 1, AR039: 0 L0748: 4, L0749: 3, H0529: 2, L0439: 2, H0624: 1, T0002: 1, H0295: 1, H0638: 1, H0619: 1, H0013: 1, H0581: 1, H0263: 1, H0457: 1, H0688: 1, H0644: 1, H0090: 1, H0551: 1, T0067: 1, H0561: 1, H0538: 1, L0500: 1, L0646: 1, L0794: 1, L0803: 1, L0790: 1, L0666: 1, L0664: 1, H0547: 1, H0690: 1, H0435: 1, H0696: 1, S0044: 1, L0779: 1, L0752: 1, L0596: 1, L0485: 1, L0593: 1 and S0384: 1.			
67	HKAEJ09	625517	77	272 - 571	1482	Ala-25 to Phe-44.	AR096: 2, AR055: 2, AR089: 1, AR104: 1, AR061: 0, AR033: 0, AR060: 0, AR052: 0,			79-95

							AR039: 0, AR053: 0 H0083: 1, H0494: 1, L0776: 1, L0744: 1 and L0777: 1.			
68	HKMMS65	625566	78	22 - 414	1483	Tyr-49 to Arg-55.	AR033: 7, AR089: 5, AR060: 4, AR039: 3, AR055: 3, AR053: 3, AR061: 3, AR052: 3, AR096: 2, AR104: 1 H0265: 2, H0431: 2, H0486: 2, H0004: 2, H0624: 1, H0716: 1, H0657: 1, S0222: 1, H0083: 1, S0214: 1, H0628: 1, L0809: 1, H0547: 1, L0748: 1, L0439: 1, L0749: 1, L0485: 1 and H0543: 1.			56-72, 18-34
69	HNHGE09	625622	79	92 - 517	1484	Pro-13 to His-18, Pro-20 to Lys-27, Ala-29 to Pro-47, Lys-69 to Arg-75, Ser-77 to Ser-85.	AR096: 2, AR089: 1, AR039: 1, AR033: 1, AR061: 1, AR104: 0, AR060: 0, AR052: 0, AR055: 0 S0053: 2			46-64
70	HTTCT34	626178	80	44 - 361	1485	Phe-42 to Tyr-50.	AR055: 6, AR061: 3, AR052: 3, AR060: 3, AR096: 3, AR033: 3, AR053: 2, AR089: 2, AR039: 2, AR104: 1 H0040: 3			50-70, 20-42

71	HBIAS14	637714	81	751 - 1185	1486	Arg-133 to Lys-145.	AR033: 164, AR055: 129, AR061: 128, AR060: 117, AR089: 90, AR039: 62, AR052: 41, AR104: 40, AR053: 30, AR096: 23 L0805: 9, S0010: 2, S6024: 1, S0134: 1, H0733: 1, S0132: 1, H0592: 1, T0048: 1, S0474: 1, S0049: 1, H0196: 1, H0052: 1, H0673: 1, S0450: 1, L0776: 1, L0809: 1, H0723: 1, S3012: 1, S3014: 1, L0743: 1, L0744: 1, L0748: 1, L0758: 1 and L0599: 1.			7-27, 114-130, 88-104, 31-47, 61-77
72	HLHSC60	638175	82	354 - 722	1487		AR096: 35, AR089: 31, AR104: 25, AR060: 17, AR033: 16, AR052: 15, AR039: 14, AR053: 13, AR055: 10, AR061: 6 H0556: 3, H0208: 3, H0050: 3, L0471: 3, H0179: 3, H0644: 3, S0344: 3, H0521: 3, L0439: 3, S0420: 2, S0360: 2, H0619: 2, H0599: 2, H0264: 2, H0280: 2, S0210: 2, H0547: 2, H0658: 2, L0750: 2, L0731: 2, L0588: 2, L0604: 2, H0543: 2, H0265: 1, T0002:			86-105, 12-29, 55-71

73	H6ESA95	638229	83	427 - 894	1488	Gln-7 to Arg-12, Pro-69 to Glu-76,	1, H0140: 1, S0114: 1, H0341: 1, S0001: 1, H0669: 1, H0662: 1, H0306: 1, S0418: 1, S0408: 1, H0580: 1, L0717: 1, H0549: 1, H0453: 1, H0592: 1, H0497: 1, H0632: 1, T0039: 1, T0112: 1, H0575: 1, H0036: 1, H0309: 1, H0544: 1, H0172: 1, H0123: 1, H0620: 1, H0024: 1, H0051: 1, H0188: 1, H0615: 1, H0604: 1, H0031: 1, L0456: 1, H0124: 1, H0376: 1, S0036: 1, H0059: 1, H0100: 1, T0041: 1, T0042: 1, S0440: 1, S0150: 1, H0646: 1, H0538: 1, L0637: 1, L0551: 1, L0803: 1, L0659: 1, L0789: 1, L0663: 1, L0438: 1, H0520: 1, H0519: 1, S0126: 1, H0689: 1, H0651: 1, H0539: 1, S0152: 1, S0028: 1, L0748: 1, L0777: 1, L0753: 1, H0343: 1, L0591: 1, L0592: 1, L0593: 1, H0423: 1, H0422: 1, H0506: 1 and H0008: 1.	AR055: 17, AR033: 17, AR052: 13, AR061: 13,		136-153, 18-34

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74	HKMAA36	638339	84	169 - 888	1489	Lys-126 to Phe-135, Asn-153 to Ala-168, Thr-185 to Val-196.	H0691: 1, H0435: 1, H0436: 1, H0478: 1, L0750: 1, L0731: 1, L0757: 1, H0445: 1, L0601: 1, H0653: 1, H0543: 1 and S0424: 1.				78-112, 1-36, 49-77, 213-232, 105-121, 29-45
							AR104: 504, AR061: 378, AR060: 336, AR055: 296, AR033: 203, AR039: 173, AR089: 171, AR052: 122, AR053: 103, AR096: 94 S0358: 11, H0494: 9, S0354: 7, S0442: 6, H0593: 6, S0444: 5, S0408: 3, H0370: 3, H0039: 3, S0434: 3, H0616: 2, H0059: 2, L0518: 2, S0374: 2, H0435: 2, H0696: 2, L0596: 2, H0484: 1, S0376: 1, S0360: 1, H0042: 1, H0292: 1, H0328: 1, H0673: 1, S0015: 1, S0440: 1, H0647: 1, L0809: 1, H0689: 1, H0672: 1, S0044: 1, S0406: 1, L0601: 1, H0506: 1 and L0600: 1.				
75	HLTFA02	638553	85	259 - 996	1490	Lys-5 to Thr-16, Thr-23 to His-28, Gly-111 to Leu-121, Pro-128 to Ile-137.	AR039: 2, AR052: 1, AR033: 1, AR055: 1, AR089: 1, AR104: 1, AR096: 1, AR061: 1,				191-207, 139-155

						AR060: 1, AR053: 0 L0747: 6, L0766: 4, L0749: 4, L0362: 4, H0046: 3, L0666: 3, S0126: 3, S0132: 2, H0013: 2, L0758: 2, L0596: 2, H0624: 1, H0341: 1, S0001: 1, S0360: 1, S0408: 1, S0278: 1, H0370: 1, T0114: 1, H0083: 1, H0553: 1, H0606: 1, H0090: 1, H0038: 1, H0616: 1, H0269: 1, H0059: 1, H0561: 1, H0641: 1, S0142: 1, L0520: 1, L0641: 1, L0764: 1, L0805: 1, L0526: 1, L0664: 1, H0702: 1, H0659: 1, H0658: 1, H0660: 1, H0666: 1, S0330: 1, H0539: 1, H0696: 1, S0406: 1, S3014: 1, S0027: 1, L0777: 1, L0755: 1, L0731: 1, L0759: 1, L0589: 1, H0136: 1, H0422: 1 and S0452: 1.			180-210, 257-282, 326-349, 116-134, 308-325, 12-28
76	HISBE12	645267	86	48 - 1193	1491	Leu-50 to Lys-58, Lys-64 to Leu-71, His-89 to Thr-94, Pro-102 to Trp-110, Tyr-162 to Cys-169, Asp-367 to Ala-377.	AR060: 6, AR096: 5, AR089: 5, AR052: 5, AR053: 3, AR033: 3, AR055: 1, AR061: 1, AR104: 1, AR039: 0 H0539: 8, H0046: 3,			

							H0039: 2, H0553: 2, H0090: 2, L0750: 2, L0605: 2, S0282: 1, H0431: 1, H0036: 1, H0421: 1, H0196: 1, T0003: 1, S6028: 1, H0252: 1, H0031: 1, H0111: 1, H0591: 1, H0412: 1, T0068: 1, S0044: 1, L0752: 1, H0445: 1 and L0581: 1.			19-51, 100-116, 120-136, 41-57
77	HBBAE43	645268	87	62 - 520	1492	Glu-9 to Arg-15, Pro-71 to Lys-79.	AR104: 44, AR033: 31, AR061: 18, AR060: 15, AR055: 14, AR039: 12, AR089: 12, AR096: 10, AR053: 9, AR052: 6 S0007: 3, H0038: 2, S0344: 2, L0750: 2, T0002: 1, H0125: 1, S0420: 1, S0358: 1, S0046: 1, H0411: 1, S0278: 1, H0085: 1, H0545: 1, H0031: 1, H0182: 1, H0646: 1, H0134: 1, S0031: 1, L0591: 1, H0423: 1 and H0422: 1.			
78	HSBBC07	655007	88	158 - 646	1493	Met-1 to Val-12.	AR053: 51, AR052: 50, AR089: 25, AR055: 25, AR033: 17, AR061: 14, AR060: 12, AR096: 12, AR104: 1, AR039: 0			117-133

79	HL2AE73	655590	89	18 - 329	1494	Pro-16 to Lys-21.	AR055: 10, AR060: 9, AR096: 8, AR053: 8, AR039: 8, AR089: 7, AR104: 7, AR061: 6, AR052: 5, AR033: 5 H0131: 2, S0002: 2, H0664: 1, H0586: 1, H0574: 1, H0563: 1, H0028: 1 and S0428: 1.			78-95, 1-17, 52-68
80	HE2OO57	656211	90	344 - 18	1495	Val-7 to Met-23, Leu-41 to Lys-46.	AR052: 30, AR053: 25, AR096: 23, AR055: 18, AR089: 16, AR060: 12, AR033: 10, AR061: 8, AR104: 6, AR039: 5 L0756: 2, H0170: 1, H0441: 1, S0051: 1, T0010: 1, H0436: 1 and L0779: 1.			89-107
81	HEEAR13	656288	91	51 - 395	1496	Asp-14 to Leu-22.	AR055: 44, AR039: 39, AR053: 24, AR033: 20, AR052: 18, AR089: 17, AR104: 16, AR096: 14, AR060: 13, AR061: 12 L0748: 5, L0157: 3, L0777: 2, H0549: 1, H0617: 1, L0638: 1, L0774: 1, L0775: 1, H0144: 1 and L0755: 1.			23-68, 23-41
82	HFIYL13	656815	92	228 - 722	1497	Gln-18 to Tyr-24, Gln-94 to Glu-100.	AR039: 8, AR033: 5, AR053: 5, AR096: 4,			131-151, 64-80, 34-

							AR052: 4, AR104: 4, AR089: 4, AR055: 3, AR060: 3, AR061: 3 L0766: 3, H0413: 2, L0794: 2, H0659: 2, H0591: 1, T0042: 1, H0494: 1, L0769: 1, L0667: 1, L0800: 1, L0662: 1, L0666: 1, H0658: 1, L0748: 1, L0755: 1, L0731: 1, L0758: 1, H0444: 1, S0242: 1 and H0542: 1.			50
83	HLWBH14	658066	93	102 - 542	1498		AR039: 34, AR053: 20, AR096: 17, AR033: 16, AR052: 16, AR104: 15, AR089: 14, AR055: 11, AR060: 11, AR061: 8 L0754: 9, L0780: 3, L0755: 3, L0591: 3, S0196: 3, H0255: 2, H0306: 2, H0041: 2, H0553: 2, H0674: 2, H0521: 2, L0748: 2, L0779: 2, L0752: 2, L0753: 2, H0445: 2, L0589: 2, S0298: 1, H0346: 1, S0360: 1, S0408: 1, H0549: 1, H0550: 1, H0485: 1, H0428: 1, H0628: 1, H0551: 1, S0142: 1, L0369: 1, L0769: 1, L0761: 1, L0800: 1,			46-62

							L0803: 1, L0782: 1, L0791: 1, L0532: 1, L0777: 1, H0444: 1, L0596: 1, S0026: 1 and H0653: 1.			52-74, 34-50, 75-91
84	HATDW51	659283	94	579 - 878	1499		AR033: 7, AR053: 4, AR055: 4, AR052: 3, AR096: 3, AR089: 3, AR060: 3, AR061: 2, AR039: 2, AR104: 1 L0766: 4, L0758: 4, L0646: 2, L0805: 2, H0670: 2, L0745: 2, L0756: 2, L0759: 2, H0351: 1, H0156: 1, H0328: 1, H0652: 1, L0520: 1, L0771: 1, L0648: 1, L0794: 1, L0774: 1, L0438: 1, L0439: 1, L0740: 1, L0747: 1 and S0412: 1.			
85	HDPWQ69	659380	95	22 - 444	1500	Phe-68 to Ser-77, Lys-79 to Thr-90, Cys-107 to Leu-114, Pro-116 to Trp-121, Pro-124 to Asn-133.	AR052: 29, AR053: 25, AR096: 23, AR089: 12, AR055: 8, AR033: 6, AR061: 4, AR060: 4, AR104: 0, AR039: 0 L0805: 25, L0157: 7, L0776: 7, S0474: 5, L0731: 5, H0457: 4, L0748: 4, L0747: 4, S0278: 3, H0538: 3, S0404: 3, S0476: 2, H0619: 2, H0009: 2, H0529:		47-64

86	HNTBM67	659801	96	231 - 1058	1501	Pro-8 to Ala-14, Glu-68 to Gln-75, Gln-80 to Glu-85,	AR053: 1, AR055: 1, AR060: 1, AR033: 1, AR096: 0, AR061: 0,	2, L0662: 2, L0803: 2, L0774: 2, L0439: 2, L0751: 2, H0170: 1, H0713: 1, H0716: 1, H0295: 1, H0341: 1, S0001: 1, H0663: 1, H0306: 1, H0402: 1, S0418: 1, L0005: 1, S0358: 1, S6016: 1, S0222: 1, H0587: 1, T0060: 1, H0427: 1, H0575: 1, T0048: 1, H0085: 1, H0178: 1, H0620: 1, S0388: 1, H0628: 1, H0674: 1, S0036: 1, H0488: 1, H0412: 1, S0038: 1, H0561: 1, H0646: 1, S0426: 1, L0598: 1, L0770: 1, L0769: 1, L0638: 1, L0639: 1, L0761: 1, L0667: 1, L0648: 1, L0794: 1, L0804: 1, L0775: 1, L0655: 1, L0809: 1, L0791: 1, L0663: 1, H0520: 1, H0689: 1, H0670: 1, S0380: 1, H0521: 1, H0522: 1, S0027: 1, L0754: 1, L0779: 1, L0777: 1, L0758: 1, S0194: 1, H0423: 1 and H0352: 1.		252-268, 133-149, 106-122

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87	HAIDY03	660532	97	37 - 537	1502	Met-1 to Lys-7,	AR055: 31, AR060: 21,						58-75

88	HDPDO12	661436	98	376 - 35	1503	Pro-9 to Ser-19, Pro-30 to Ser-38, Arg-89 to Glu-95, Leu-105 to Trp-113, Lys-124 to Thr-129.	Thr-107 to Asn-114.	AR033: 20, AR061: 15, AR089: 13, AR053: 12, AR052: 11, AR104: 7, AR096: 6, AR039: 4 L0766: 5, L0803: 3, L0748: 3, L0740: 3, L0758: 3, S0408: 2, H0032: 2, H0124: 2, L0771: 2, L0809: 2, L0665: 2, S0330: 2, L0750: 2, L0756: 2, L0731: 2, L0759: 2, H0254: 1, H0638: 1, S0420: 1, S0358: 1, S0132: 1, H0013: 1, S0010: 1, H0563: 1, H0510: 1, H0416: 1, H0687: 1, S0003: 1, H0328: 1, H0591: 1, H0413: 1, H0207: 1, H0538: 1, S0422: 1, S0426: 1, L0763: 1, L0769: 1, L0796: 1, L0667: 1, L0643: 1, L0648: 1, L0794: 1, L0805: 1, L0776: 1, L0655: 1, L0783: 1, L0367: 1, L0664: 1, H0144: 1, H0519: 1, H0690: 1, H0658: 1, H0672: 1, H0518: 1, H0696: 1, S0044: 1, L0439: 1, L0747: 1, L0752: 1, S0192: 1 and H0422: 1.	AR096: 3, AR053: 3,			44-72, 69-

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89	HAGBC45	661694	99	51 - 860	1504	Pro-29 to Lys-34, Ser-91 to Thr-97.	AR055: 6, AR033: 4, AR096: 3, AR052: 3, AR061: 3, AR089: 3, AR060: 3, AR053: 3, AR039: 2, AR104: 0 L0777: 7, L0750: 6, L0748: 5, L0779: 4, L0805: 2, L0517: 2, L0439: 2, L0740: 2, L0747: 2, L0759: 2, H0580: 1, S0010: 1, T0003: 1, H0622: 1, S0036: 1, L0764: 1, L0803: 1, H0144: 1, S3014: 1, L0749: 1 and L0758: 1.			179-199
90	HNTNT65	662513	100	85 - 480	1505	Val-4 to Thr-11, Ile-15 to Asn-20, Arg-35 to Lys-44.	AR089: 3, AR053: 3, AR052: 2, AR096: 2, AR104: 2, AR039: 2, AR055: 2, AR033: 2, AR060: 1, AR061: 1 H0651: 8, L0744: 7,			50-70

	L0748: 6, H0620: 4, S0360: 3, S0142: 3, L0755: 3, H0638: 2, H0052: 2, H0123: 2, H0083: 2, H0328: 2, H0615: 2, H0039: 2, H0424: 2, H0163: 2, H0040: 2, H0059: 2, L0659: 2, L0519: 2, L0438: 2, S0378: 2, S3012: 2, S3014: 2, L0743: 2, L0750: 2, L0758: 2, L0589: 2, H0656: 1, H0662: 1, S0420: 1, S0358: 1, S0408: 1, H0637: 1, S0222: 1, H0574: 1, S0280: 1, L0021: 1, H0544: 1, H0546: 1, H0545: 1, H0081: 1, H0012: 1, H0266: 1, H0188: 1, H0687: 1, H0288: 1, H0292: 1, H0252: 1, H0673: 1, S0036: 1, H0100: 1, H0641: 1, S0144: 1, S0002: 1, L0761: 1, L0643: 1, L0662: 1, L0650: 1, L0774: 1, L0375: 1, L0805: 1, L0776: 1, L0783: 1, L0793: 1, L0665: 1, S0053: 1, H0520: 1, H0658: 1, H0672: 1, H0522: 1, S0406: 1, H0436: 1, S0037: 1, L0747: 1, L0749: 1, L0779: 1,						

							L0731: 1, S0031: 1, S0434: 1 and L0366: 1.			
91	HTTAA50	665234	101	825 - 1148	1506	Asn-87 to Asn-92.	AR096: 6, AR052: 4, AR060: 4, AR055: 4, AR033: 4, AR039: 4, AR104: 3, AR089: 3, AR053: 3, AR061: 3 L0766: 4, L0748: 4, L0747: 4, L0752: 3, L0759: 3, S0212: 1, S0356: 1, H0574: 1, L0105: 1, H0188: 1, H0040: 1, L0772: 1, L0774: 1, S0328: 1, L0749: 1, L0755: 1, L0596: 1 and H0667: 1.	6q22.1-22.3	120110, 121014, 142470, 156225, 164200, 164200, 601316, 601410, 601757	8-35, 38-56, 59-75
92	HAGBX32	666416	102	102 - 512	1507	Pro-27 to Ala-37.	AR033: 8, AR053: 5, AR052: 5, AR089: 5, AR060: 4, AR096: 4, AR055: 3, AR104: 3, AR061: 3, AR039: 1 L0439: 4, L0418: 1, S0010: 1, L0455: 1, S0028: 1 and L0741: 1.	16p12-p13.1	108730, 147781, 172471, 186580, 264800, 266600, 278760, 600760, 600760, 600761, 600761, 602066	45-69, 76-101, 115-131
93	HHTMM18	666429	103	112 - 543	1508	Glu-98 to Gln-106.	AR089: 28, AR039: 26, AR096: 25, AR052: 16,			41-57

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94	HHFGR08	667779	104	296 - 625	1509	Ser-14 to Arg-20, Pro-92 to Ala-97, Glu-104 to His-110.	AR052: 3, AR053: 3, AR033: 2, AR055: 2, AR104: 1, AR096: 1, AR061: 1, AR060: 1, AR089: 1, AR039: 0 S0422: 7, L0748: 6, L0664: 4, H0581: 3, L0665: 3, H0038: 2, H0659: 2, L0743: 2, L0751: 2, S0434: 2, L0596: 2, L0592: 2, L0411: 1, H0556: 1, H0222: 1, H0656: 1, S0116: 1, S0358: 1, S0376: 1, S0444: 1, S0360: 1, S0132: 1, S0476: 1, H0497: 1, H0013: 1, H0050: 1, H0375: 1, H0622: 1, H0591: 1, H0040: 1, S0142: 1, S0002: 1, L0643: 1, L0662: 1, L0794: 1, L0766: 1, L0791: 1, H0547: 1, H0519: 1, H0518: 1, H0521: 1, L0749: 1, L0777: 1 and H0422: 1.			
95	HHBEU19	668286	105	26 - 469	1510	Ala-62 to Glu-74.	AR096: 1, AR060: 0, AR033: 0, AR061: 0,			123-139

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96	HWBBB21	670586	106	34 - 627	1511	Tyr-35 to Gln-42, Asp-141 to Gly-160.	AR096: 7, AR053: 5, AR039: 5, AR060: 3, AR052: 3, AR104: 3, AR089: 3, AR033: 2, AR061: 1, AR055: 0 H0580: 1, T0042: 1, S0002: 1 and L0439: 1.			59-75, 1-17, 104-120, 169-185
97	HAIDX85	672653	107	246 - 1880	1512	Arg-54 to Trp-62, Pro-68 to Ile-77, Asn-124 to Ala-130, Arg-155 to Lys-161, Ser-166 to Glu-178, Ile-407 to Ser-413, Pro-494 to Met-507, Pro-510 to Asp-516.	AR033: 8, AR055: 7, AR060: 6, AR089: 4, AR052: 4, AR061: 3, AR096: 3, AR053: 2, AR104: 1, AR039: 1 H0038: 4, H0124: 2, H0561: 2, H0539: 2, S0276: 2, H0294: 1, S0212: 1, S0132: 1, H0431: 1, S0005: 1, H0544: 1, H0123: 1, H0266: 1, H0288: 1, H0039: 1, H0040: 1, H0547: 1, H0519: 1, S0044: 1, H0555: 1 and S0242: 1.			370-406, 10-38, 430-456, 262-279, 338-354, 303-320, 232-250, 476-492, 105-121, 180-196
98	HMMAV06	675380	108	10 - 618	1513		AR096: 4, AR089: 2, AR053: 2, AR052: 2,			54-71

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99	HISAM25	677920	109	291 - 680	1514	Ile-52 to Ser-59, Arg-106 to Asn-111, Gln-122 to Lys-130.	AR033: 3, AR104: 2, AR096: 2, AR053: 2, AR039: 2, AR089: 1, AR052: 1, AR060: 1, AR061: 1, AR055: 0 L0769: 3, L0747: 3, L0759: 3, L0783: 2, L0438: 2, H0539: 2, L0439: 2, L0758: 2, L0589: 2, L0717: 1, L0598: 1, L0520: 1, L0794: 1, L0375: 1, H0144: 1 and L0779: 1.			
100	HRODX93	678316	110	408 - 725	1515	Pro-13 to Arg-23.	AR053: 52, AR052: 44, AR055: 40, AR104: 28, AR033: 28, AR089: 27, AR060: 23, AR061: 22,			59-75, 84-100, 23-39

101	HLJDK82	678819	111	238 - 1713	1516	Asp-23 to Glu-28, Ser-49 to Pro-54, Glu-61 to Thr-67, Glu-72 to Asp-81, Glu-83 to Asp-118, Gly-156 to Arg-162, Asp-184 to Tyr-205, Met-251 to Asp-257, Gln-273 to Asp-278, Ser-284 to Tyr-293, Phe-333 to Ser-338, Lys-351 to Arg-357, Gly-367 to Asp-375, Asn-399 to Glu-414, Gln-424 to Arg-443, Glu-447 to Glu-457, Arg-462 to Lys-476, Lys-485 to Phe-492.	AR096: 22, AR039: 20 H0052: 1 and H0598: 1.			137-155, 1-19
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102	HCFMJ37	682668	112	164 -	1517		AR033: 5, AR089: 4,			73-90, 12-

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103	HMWAPI 7	682949	113	373 - 26	1518		AR055: 15, AR039: 14, AR089: 12, AR052: 12, AR033: 11, AR060: 10, AR053: 9, AR061: 9, AR104: 8, AR096: 7 H0666: 13, H0620: 7, L0731: 7, L0747: 6, L0659: 5, L0740: 5, L0750: 5, L0757: 5, S0360: 4, H0123: 4, S0022: 4, H0135: 4, L0666: 4, L0665: 4, S0028: 4, L0748: 4, L0777: 4, L0588: 4, S0420: 3, S0358: 3, H0208: 3, H0545: 3, H0046: 3, H0284: 3, L0650: 3, L0375: 3, L0382: 3, H0352: 3, H0592: 2, H0544: 2, H0024: 2, H0266: 2, H0286: 2, H0252: 2, H0428: 2, H0628: 2, H0551: 2, H0100: 2, S0210: 2, L0763: 2, L0770: 2, L0774: 2, L0661: 2, L0518: 2, H0547: 2, H0670: 2, S0037: 2, L0751: 2, L0752: 2, L0755:			87-105, 31-47

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104	HMCFA76	684293	114	34 - 519	1519	Ala-4 to Phe-9, Thr-155 to Asn-162.	1 and H0667: 1. AR055: 25, AR052: 25, AR053: 22, AR033: 18, AR089: 18, AR060: 15, AR096: 15, AR039: 15, AR061: 14, AR104: 14 L0758: 7, L0766: 5, L0558: 5, L0750: 5, S0360: 4, S0410: 4, L0747: 4, S0007: 3, S0438: 3, L0763: 3, L0769: 3, L0775: 3, S0380: 3, S0404: 3, L0748: 3, L0754: 3, L0749: 3, L0759: 3, H0423: 3, H0661: 2, S0132: 2, H0441: 2, H0494: 2, L0506: 2, L0761: 2, L0554: 2, L0523: 2, L0776: 2, L0526: 2, L0532: 2, L0665: 2, S0126: 2, S0378: 2, H0522: 2, L0742: 2, L0752: 2, L0731: 2, L0757: 2, S0040: 1, H0717: 1, H0294: 1, S0134: 1, H0657: 1, H0381: 1, H0341: 1, H0483: 1, H0669: 1, H0638: 1, S0358: 1, S0444: 1, S0408: 1, H0208: 1, H0351: 1, S0278: 1, H0392: 1, H0333: 1, L0622: 1, H0486: 1, T0039: 1, L0021:			92-120, 117-133, 30-50, 61-77

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105	HTHCM28	684309	115	145 - 1392	1520	Pro-29 to Asn-35, Val-184 to Arg-191, Thr-219 to Thr-225, Ala-273 to Ser-281,	AR055: 11, AR052: 10, AR033: 8, AR060: 7, AR061: 7, AR089: 7, AR053: 6, AR096: 5,						

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106	HHEDB45	685054	116	180 - 623	1521	Thr-2 to Glu-13, Asn-19 to His-56, His-140 to Pro-148.	H0423: 1. AR039: 6, AR096: 4, AR033: 4, AR053: 4, AR104: 3, AR052: 3, AR089: 3, AR060: 3, AR055: 2, AR061: 2 H0170: 1, H0484: 1, S0360: 1, H0309: 1, H0040: 1, L0611: 1, L0596: 1, H0542: 1 and H0543: 1.	12p12	112410, 113520, 135700, 168470, 186940, 186940, 200990, 602096	70-86
107	HTACX15	685191	117	75 - 965	1522		AR060: 5, AR052: 5, AR089: 4, AR053: 4, AR096: 3, AR055: 3, AR033: 2, AR039: 2, AR061: 2, AR104: 1 L0779: 4, S0360: 3, L0803: 3, L0747: 3, L0758: 3, S0354: 2, H0637: 2, S0422: 2, L0646: 2, L0519: 2, L0665: 2, H0436: 2, L0750: 2, H0657: 1, S0007: 1, S6016: 1, H0415: 1, H0486: 1, H0069: 1, H0427: 1, S0280: 1, H0118: 1, H0014: 1, S0214: 1, H0328: 1, H0615: 1, H0553: 1, H0628: 1, S0440: 1, H0529: 1, L0766: 1, L0650: 1, L0775: 1, L0776: 1, L0655:		47-66, 275-291, 146-162, 99-115

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108	HFIZN55	685340	118	324 - 713	1523		AR089: 2, AR039: 1, AR055: 1, AR096: 1, AR053: 1, AR104: 1, AR060: 0, AR061: 0, AR033: 0, AR052: 0 L0805: 2, L0749: 2, H0024: 1, H0112: 1, L0803: 1, H0660: 1, S0330: 1, L0748: 1, L0747: 1 and S0242: 1.			
109	HCE1U38	685495	119	24 - 1067	1524	Pro-89 to Gly-96, Gly-119 to Leu-125, Thr-135 to Pro-141, Thr-160 to Arg-170, Glu-189 to Glu-196, Asp-229 to Asp-236, Arg-278 to His-286, Asn-337 to Tyr-348.	AR089: 8, AR055: 7, AR039: 6, AR033: 6, AR052: 6, AR060: 6, AR096: 5, AR061: 5, AR053: 5, AR104: 4 L0747: 14, L0439: 11, L0731: 8, L0438: 6, L0769: 5, L0766: 5, L0809: 5, L0749: 5, H0251: 4, H0124: 4, H0052: 3, H0545: 3, L0770: 3, L0804: 3, L0774: 3, L0776: 3, L0659: 3, L0663: 3, H0547: 3, L0748: 3, L0757: 3, L0758: 3,			301-338, 16-32

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110	HNFIL36	685604	120	256 - 735	1525	AR089: 0, AR096: 0, AR060: 0, AR061: 0, AR104: 0, AR055: 0, AR052: 0, AR039: 0 L0517: 4, L0769: 3, L0776: 3, L0790: 3, L0743: 2, L0754: 2, H0341: 1, S0442: 1, S0046: 1, S0140: 1, S0132: 1, H0550: 1, H0036: 1, L0031: 1, H0271: 1, H0416: 1, H0428: 1, H0031: 1, L0142: 1, H0617: 1, L0761: 1, L0764: 1, L0805: 1, L0659: 1, H0691: 1, H0519: 1, S0378: 1, H0436: 1, L0748: 1, L0777: 1, L0755: 1, L0758: 1 and L0697: 1.			
111	HSKZB03	686533	121	1521 - 1096	1526	Glu-10 to Thr-15, Arg-33 to Glu-38, Leu-54 to Gly-59,	AR096: 4, AR055: 3, AR061: 3, AR060: 3, AR053: 3, AR052: 3,			62-78, 105-121

112	HNTMZ26	688935	122	12 - 416	1527	Gly-86 to Trp-101, Pro-123 to Thr-133.	AR089: 2, AR033: 2, AR104: 2, AR039: 0 S0126: 8, S0420: 6, L0757: 6, S0212: 4, L0777: 4, H0662: 3, L0743: 3, L0608: 3, H0653: 3, H0667: 3, H0546: 2, S0314: 2, H0551: 2, L0564: 2, L0764: 2, L0666: 2, H0660: 2, S0027: 2, L0740: 2, L0754: 2, L0759: 2, L0591: 2, L0595: 2, H0665: 2, S0180: 1, H0661: 1, S0418: 1, S0356: 1, T0007: 1, T0039: 1, T0040: 1, T0114: 1, H0013: 1, L0021: 1, H0599: 1, H0036: 1, H0083: 1, L0669: 1, S0318: 1, S0316: 1, H0284: 1, H0286: 1, S0340: 1, S0250: 1, H0553: 1, S0364: 1, H0413: 1, H0494: 1, S0150: 1, L0763: 1, L0775: 1, L0776: 1, L0657: 1, L0790: 1, H0689: 1, H0690: 1, H0658: 1, S3012: 1, S0037: 1, S3014: 1, S0028: 1, L0780: 1, L0731: 1, H0668: 1, S0194: 1 and S0196: 1.	Leu-27 to Ser-41.	AR039: 5, AR089: 3,		102-122

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114	HHSGJ30	691490	124	110 - 427	1529	Ser-25 to Lys-32, Glu-63 to Gly-68.	AR039: 31, AR033: 26, AR104: 25, AR053: 22, AR052: 19, AR055: 19, AR089: 14, AR060: 13, AR096: 11, AR061: 10 L0439: 3, L0438: 2, L0756: 2 and S0388: 1.				
115	HE8EQ09	695741	125	135 - 1184	1530	Gln-153 to Ser-163, Ser-172 to Glu-178, Ala-204 to Asp-210, Ile-222 to Ala-236, Lys-284 to Ser-291, Met-342 to Arg-348.	AR033: 29, AR104: 25, AR060: 22, AR096: 17, AR089: 16, AR052: 13, AR039: 11, AR055: 9, AR053: 8, AR061: 5 L0752: 30, L0754: 17, L0740: 16, H0521: 14, L0439: 14, L0766: 12, S0003: 11, S0214: 11, L0777: 10, S0002: 8, L0776: 8, L0748: 8, L0755: 8, S0360: 7, L0665: 7, L0757: 7, T0067: 6, S0440: 6, L0770: 6, L0666: 6, L0747: 6, L0774: 5, L0751: 5, S0222: 4, H0575: 4, H0622: 4, L0662: 4, L0775:	X		300-328, 1-21, 180-196

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116	HJKSC77	698634	126	26 - 499	1531	Ala-8 to Ser-15, His-36 to Glu-44,	1, H0438: 1, H0013: 1, S0010: 1, S0665: 1, S0474: 1, H0327: 1, H0046: 1, L0157: 1, S0051: 1, T0010: 1, H0266: 1, H0179: 1, H0615: 1, H0096: 1, H0031: 1, H0553: 1, L0055: 1, H0674: 1, H0163: 1, H0038: 1, H0264: 1, H0413: 1, L0564: 1, H0560: 1, H0359: 1, H0509: 1, S0142: 1, S0344: 1, UNKWN: 1, L0369: 1, L0762: 1, L0371: 1, L0796: 1, L0761: 1, L0373: 1, L0773: 1, L0521: 1, L0794: 1, L0803: 1, L0804: 1, L0784: 1, L0807: 1, L0518: 1, L0647: 1, L5622: 1, L5623: 1, H0144: 1, H0684: 1, H0659: 1, H0658: 1, S0330: 1, S0152: 1, H0696: 1, S0404: 1, S0037: 1, L0746: 1, L0779: 1, S0031: 1, H0707: 1, S0434: 1, L0480: 1, L0608: 1, L0604: 1, S0011: 1, S0192: 1, S0456: 1 and H0506: 1.	AR033: 7, AR052: 6, AR104: 5, AR060: 5,			139-158, 110-126

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117	HDABD32	699216	127	154 - 471	1532	Met-1 to Lys-6, Glu-52 to Thr-58, His-72 to Ala-77.	AR052: 4, AR096: 3, AR053: 3, AR089: 2, AR104: 2, AR033: 2, AR060: 2, AR039: 2, AR055: 1, AR061: 1 L0766: 10, L0794: 6, L0439: 6, L0731: 5, L0779: 4, H0622: 2, S0422: 2, L0740: 2, L0756: 2, L0595: 2, H0402: 1, S0420: 1, S0444: 1, H0580: 1, H0208: 1, L0717: 1, S0278: 1, H0261: 1, S0222: 1, H0497: 1, H0574: 1, L0471: 1, H0553: 1, H0641: 1, L0646: 1, L0764: 1, L0773: 1, L0803: 1, L0804: 1, L0526: 1, L0791: 1, L0664: 1, L0665: 1, H0520: 1, H0521: 1, H0522: 1, H0696: 1, H0436: 1, L0777: 1, L0755: 1, L0759: 1, H0595: 1, L0604: 1, H0543: 1 and H0422: 1.				
118	HWACC64	702658	128	350 - 694	1533		AR052: 2, AR053: 2, AR039: 1, AR055: 1,				12-34, 98-114

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119	HMWTW46	703503	129	534 - 1145	1534	Glu-49 to Gln-55, Asn-115 to Gln-136, Glu-154 to Asn-169, Ser-183 to Asn-191.	AR055: 10, AR052: 9, AR053: 7, AR060: 6, AR061: 5, AR033: 5, AR096: 5, AR104: 5, AR089: 4, AR039: 3 L0766: 13, L0749: 8, L0776: 6, L0803: 5, L0770: 4, L0805: 4, H0100: 3, L0794: 3, L0789: 3, L0748: 3, L0745: 3, L0779: 3, L0777: 3, T0002: 2, H0090: 2, L0800: 2, L0809: 2, H0134: 2, L0756: 2, L0752: 2, L0758: 2, L0605: 2, H0170: 1, H0556: 1, H0341: 1, H0192: 1, S0476: 1, H0549: 1, S0222: 1, H0587: 1, H0013: 1, H0575: 1, T0103: 1, H0046: 1, H0067: 1, H0266: 1, H0284: 1, T0042: 1, L0796: 1, L0761: 1, L0363: 1, L0768: 1,	L0655: 1, L0607: 1, L0661: 1, L0659: 1, L0809: 1, L0787: 1, L0664: 1, S0052: 1, S0053: 1, H0698: 1, H0701: 1, S0330: 1, S0378: 1, H0521: 1, H0214: 1, L0756: 1, L0779: 1, L0777: 1, L0755: 1 and H0136: 1.		

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120	HSDIJ72	705030	130	242 - 646	1535	AR052: 23, AR055: 16, AR053: 14, AR096: 10, AR089: 9, AR060: 8, AR061: 7, AR033: 6, AR039: 4, AR104: 4 L0747: 5, L0749: 5, L0764: 3, L0804: 3, L0755: 3, S0360: 2, H0135: 2, H0529: 2, H0696: 2, H0134: 2, S0406: 2, L0777: 2, L0731: 2, L0758: 2, L0362: 2, H0265: 1, H0294: 1, S0116: 1, S0418: 1, S0420: 1, S0132: 1, H0586: 1, H0333: 1, H0486: 1, H0156: 1, H0597: 1, H0178: 1, L0471: 1, H0057: 1, H0083: 1, H0594: 1, S0022: 1, T0023: 1, H0617: 1, L0055: 1, H0674: 1, H0591: 1, H0551: 1, H0413: 1, H0494: 1, H0560: 1, S0448: 1, S0440: 1, H0646: 1, L0662: 1, L0766: 1, L0649: 1,			

121	HSLGO34	706987	131	46 - 408	1536	Met-1 to Leu-6, Ala-10 to Tyr-15, Arg-65 to Gln-70, Pro-107 to Glu-116.	L0783: 1, L0383: 1, L0382: 1, L0789: 1, L0666: 1, L0663: 1, H0520: 1, S0126: 1, H0689: 1, S0390: 1, L0751: 1, L0752: 1, L0759: 1, S0031: 1, S0260: 1, S0434: 1, L0597: 1, H0667: 1 and S0424: 1.			80-99
122	HTOJF39	707266	132	214 - 519	1537		AR096: 6, AR053: 5, AR052: 5, AR055: 5, AR033: 4, AR060: 3, AR061: 3, AR089: 3, AR104: 2, AR039: 2 L0766: 7, H0521: 3, L0779: 3, H0543: 3, H0580: 2, H0509: 2, L0662: 2, L0803: 2, L0805: 2, H0519: 2, H0539: 2, L0756: 2, L0759: 2, H0542: 2, S0116: 1, S0354: 1, H0637: 1, H0574: 1, H0421: 1, S6028: 1, S0003: 1, S0214: 1,			42-59, 15-31

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123	HPDEF35	707398	133	36 - 362	1538	Ser-21 to Gly-28, Gly-36 to Arg-41, Arg-66 to Tyr-74.	AR053: 18, AR052: 17, AR055: 15, AR096: 14, AR089: 11, AR060: 9, AR061: 8, AR033: 8, AR104: 7, AR039: 5 H0457: 2, T0023: 1, H0144: 1, H0436: 1 and H0677: 1.				
124	HFIAW95	707878	134	129 - 533	1539	Arg-39 to Thr-46.	AR039: 47, AR033: 18, AR053: 16, AR104: 14, AR089: 14, AR096: 14, AR055: 11, AR052: 10, AR060: 10, AR061: 7 L0758: 4, L0731: 2, S0192: 2, H0038: 1 and L0638: 1.				77-95, 5-21
125	HMEIU36	708053	135	132 - 635	1540	Ser-108 to Gln-125, Thr-156 to Glu-166.	AR096: 20, AR039: 17, AR089: 13, AR052: 11, AR053: 10, AR055: 9, AR060: 9, AR104: 8, AR033: 8, AR061: 4 L0803: 14, S0474: 13, L0748: 13, S0408: 11,	3p21.3	116806, 120120, 120120, 120120, 120436, 120436, 120436,		51-68

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126	HHEDM89	708177	136	30 - 668	1541	Ser-76 to Ser-82.	AR053: 3, AR096: 3, AR039: 2, AR052: 2, AR104: 2, AR033: 2, AR089: 2, AR060: 1, AR055: 1, AR061: 1 L0779: 5, L0157: 2, L0803: 2, L0754: 2, L0595: 2, H0305: 1, H0589: 1, H0638: 1, H0351: 1, H0486: 1, L0021: 1, H0318: 1, H0596: 1, S0150: 1, S0144: 1, L0364: 1, L0766: 1, L0809: 1, L0532: 1, H0667: 1 and H0542: 1.				
127	HKABW60	709347	137	95 - 748	1542	Ala-16 to Glu-36, Arg-51 to Thr-56, Glu-104 to Thr-112.	AR033: 13, AR089: 12, AR060: 8, AR053: 8, AR039: 7, AR055: 6, AR052: 6, AR096: 5, AR061: 4, AR104: 3 H0038: 4, H0529: 3, L0803: 3, L0747: 3, L0779:	21q22.3	120220, 120240, 123580, 151385, 171860, 190685, 236100,		70-87

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130	HEAAK34	711111	140	7 - 825	1545		AR039: 46, AR052: 45, AR053: 36, AR096: 34, AR033: 27, AR055: 24, AR104: 24, AR089: 23, AR060: 18, AR061: 11 L0439: 3, L0438: 2, S0028: 2, H0656: 1, H0645: 1, H0369: 1, S0222: 1, S0346: 1, H0328: 1, H0029: 1, H0644: 1, H0169: 1, H0591: 1, H0646: 1, H0520: 1, H0539: 1, L0746: 1 and L0366: 1.			122-138, 90-106, 145-161
131	HLWAH41	711706	141	275 - 706	1546		AR096: 3, AR052: 2, AR039: 2, AR055: 2, AR033: 2, AR089: 2, AR060: 2, AR061: 1, AR053: 1, AR104: 1 L0748: 6, L0752: 5, H0553: 2, L0754: 2, L0749: 1 and L0780: 1.			85-117
132	HHSFI89	712570	142	40 - 369	1547	Pro-8 to Thr-16, Glu-50 to Glu-60, Gln-67 to Arg-72, Lys-81 to Asn-94.	AR089: 8, AR033: 8, AR060: 6, AR096: 2, AR061: 2, AR053: 1, AR052: 1, AR039: 0, AR104: 0 S0388: 1, H0083: 1 and L0777: 1.			93-110
133	HSAVI33	714693	143	211 -	1548	Met-1 to Arg-6,	AR052: 17, AR053: 12,			52-68, 94-

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134	HMJAX17	715359	144	662-333	1549		AR052: 5, AR096: 5, AR089: 4, AR033: 3, AR053: 3, AR055: 2, AR104: 2, AR060: 2,	22q13.33	61-79, 78-94

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135	HLJDZ45	717449	145	271 - 849	1550					
136	HAHBC57	718574	146	40 - 480	1551	Ile-95 to Ala-101, Leu-110 to Ser-128.	AR039: 76, AR052: 40, AR033: 39, AR096: 39, AR055: 38, AR104: 33, AR053: 33, AR089: 28, AR060: 24, AR061: 20 L0485: 2, S0282: 1, S0418: 1, H0002: 1, H0253: 1, H0196: 1, L0794: 1 and L0787: 1.			48-64
137	HLYDR60	718768	147	281 - 661	1552	Glu-22 to Ala-29, Ser-47 to Arg-58, Ser-108 to Tyr-113.	AR096: 1, AR052: 1, AR089: 1, AR060: 0, AR061: 0, AR033: 0, AR039: 0, AR053: 0			111-127

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138	HCHMQ09	719977	148	10 - 372	1553		AR033: 4, AR039: 3, AR096: 2, AR089: 2, AR061: 2, AR052: 1, AR060: 1, AR104: 1, AR053: 0, AR055: 0 H0484: 1, S0280: 1, H0373: 1 and H0593: 1.		
139	HADMD75	720237	149	105 - 431	1554	Arg-11 to Gly-16, Pro-35 to Phe-44.	AR033: 4, AR089: 4, AR061: 2, AR060: 1, AR052: 1, AR104: 1, AR039: 0, AR055: 0, AR096: 0, AR053: 0 L0805: 3, L0439: 3, H0674: 2, L0518: 2, L0809: 2, L0789: 2, L0751: 2, L0758: 2, H0390: 1, H0544: 1, H0570: 1, S0051: 1, T0006: 1, L0769: 1, L0800: 1, L0794: 1, L0803: 1, L0661: 1, L0636: 1, L0529:		76-99

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140	HKADW47	720269	150	51 - 473	1555	Ala-7 to Lys-28, Gly-45 to Lys-55.	AR052: 3, AR096: 3, AR033: 2, AR053: 1, AR039: 1, AR104: 1, AR055: 1, AR089: 1, AR060: 1, AR061: 1 L0794: 10, L0803: 4, S0045: 3, H0486: 3, H0013: 3, H0251: 3, H0591: 3, H0265: 2, S0360: 2, S0222: 2, H0090: 2, H0561: 2, L0809: 2, H0519: 2, L0439: 2, L0758: 2, L0591: 2, H0170: 1, H0556: 1, S0040: 1, S0114: 1, L0760: 1, H0255: 1, S0444: 1, H0432: 1, H0587: 1, H0632: 1, H0492: 1, H0575: 1, H0178: 1, H0050: 1, H0620: 1, H0688: 1, H0553: 1, L0435: 1, H0494: 1, H0641: 1, L0638: 1, L0761: 1, L0766: 1, L0774: 1, L0653: 1, L0663: 1, H0144: 1, L0438: 1, H0689: 1, H0659: 1, H0521: 1, S0146: 1, L0748:			

141	HFAUL30	721084	151	28 - 327	1556	Gly-10 to Glu-16, Gln-88 to Leu-99.	1, L0754: 1, L0747: 1, L0750: 1, L0752: 1, S0434: 1, L0595: 1 and L0366: 1.	AR055: 16, AR039: 15, AR033: 15, AR053: 13, AR052: 10, AR089: 10, AR096: 10, AR104: 9, AR060: 8, AR061: 7 L0769: 4, S0126: 4, L0758: 4, L0755: 3, S0358: 2, S0444: 2, H0617: 2, H0673: 2, L0764: 2, S0374: 2, L0748: 2, L0779: 2, L0592: 2, H0716: 1, H0656: 1, H0341: 1, S0418: 1, S0420: 1, H0675: 1, S0408: 1, H0580: 1, S0046: 1, S0300: 1, H0632: 1, H0013: 1, S0280: 1, L0043: 1, H0606: 1, H0316: 1, S0150: 1, S0344: 1, L0762: 1, L0763: 1, L0761: 1, L0771: 1, L0766: 1, L0774: 1, L0775: 1, L0375: 1, L0655: 1, L0382: 1, H0144: 1, H0690: 1, S0328: 1, H0710: 1, H0521: 1, L0744: 1, L0786: 1, L0731: 1, H0445: 1, H0667: 1, S0276: 1, H0543: 1, H0422: 1 and		62-78

142	HKADD23	721126	152	181 - 609	1557			S0446: 1. AR104: 10, AR033: 7, AR052: 6, AR089: 4, AR053: 4, AR096: 3, AR039: 3, AR060: 3, AR055: 2, AR061: 0 L0766: 4, H0494: 2, L0755: 2, S0040: 1, S0420: 1, S0046: 1, S0132: 1, S0222: 1, H0438: 1, H0250: 1, S0010: 1, H0038: 1, H0538: 1, L0800: 1, L0773: 1, H0670: 1 and L0777: 1.			70-87
143	HE8MO09	721141	153	42 - 401	1558	Leu-14 to Glu-23, Lys-41 to Arg-50, Pro-90 to Gln-96.		AR053: 42, AR096: 31, AR052: 30, AR089: 24, AR033: 23, AR104: 18, AR039: 18, AR055: 16, AR060: 16, AR061: 8 L0439: 9, H0013: 3, H0090: 2, H0561: 2, L0754: 2, L0731: 2, H0170: 1, H0341: 1, H0580: 1, H0485: 1, L0471: 1, H0024: 1, H0644: 1, H0591: 1, H0551: 1, L0766: 1, L0606: 1, L0659: 1, L0438: 1, L0352: 1, H0672: 1, H0521: 1, H0436: 1, H0627: 1, L0748: 1 and H0542: 1.			71-87

144	HE8FL67	721418	154	213 - 593	1559	Met-1 to Gly-7.	AR039: 20, AR089: 18, AR052: 18, AR053: 17, AR096: 17, AR033: 15, AR055: 15, AR104: 14, AR060: 13, AR061: 6 H0013: 1, L0761: 1 and L0779: 1.		106-127, 56-77, 80-98
145	HBOOA49	722648	155	124 - 600	1560	Met-1 to Cys-18.	AR089: 6, AR033: 5, AR060: 5, AR053: 3, AR096: 3, AR061: 2, AR052: 2, AR039: 2, AR055: 2, AR104: 1 H0617: 9, H0549: 4, S0406: 4, L0439: 3, H0717: 2, H0255: 2, S0358: 2, H0550: 2, S0049: 2, H0494: 2, L0777: 2, H0713: 1, H0716: 1, H0484: 1, S0356: 1, S0132: 1, H0619: 1, L0021: 1, H0421: 1, H0457: 1, S0366: 1, H0379: 1, S0344: 1, H0529: 1, L0639: 1, L0761: 1, L0803: 1, L0774: 1, L0657: 1, L0783: 1, L0789: 1, H0593: 1, H0539: 1, H0436: 1 and H0543: 1.		42-58, 73-89, 120-136
146	HMSJH49	722943	156	34 - 591	1561		AR055: 11, AR060: 7, AR096: 5, AR033: 5,		77-97, 14-31

147	HARAX45	723491	157	218 - 910	1562	Pro-28 to Ser-33, Pro-66 to Arg-79, Ser-163 to Gly-180.	AR052: 5, AR061: 5, AR039: 4, AR089: 3, AR053: 3, AR104: 3 L0539: 2, H0546: 1, S0386: 1, H0560: 1, S0002: 1, L0741: 1 and L0746: 1.	15q13-q14	102540, 103581, 118511, 146150, 218000, 227220, 243500, 254770, 601623, 601800, 601889, 602117		1-25, 86-119, 142-159, 79-95
148	HDTES50	724196	158	48 - 395	1563		AR096: 3, AR039: 1, AR052: 1, AR089: 1, AR060: 1, AR055: 0, AR061: 0, AR033: 0, AR053: 0, AR104: 0 H0341: 1 and H0486: 1.				89-107, 6-22
149	HKGBC30	724352	159	318 - 662	1564	Met-1 to Ala-7, His-24 to Pro-35.	AR061: 1, AR033: 1, AR039: 0, AR089: 0, AR053: 0, AR096: 0, AR055: 0, AR060: 0, AR052: 0, AR104: 0				41-58

150	HKIXO37	724432	160	90 - 500	1565	Glu-10 to Asn-15, Val-73 to Arg-83, Gly-118 to Ser-128.	AR052: 19, AR055: 18, AR089: 17, AR053: 14, AR033: 11, AR061: 9, AR060: 9, AR096: 8, AR039: 0, AR104: 0 L0766: 4, H0441: 1, L0744: 1 and L0596: 1.			90-106, 42-58
151	HTLFI39	724950	161	218 - 577	1566	Met-1 to Ser-7.	AR039: 53, AR055: 28, AR053: 27, AR033: 23, AR052: 21, AR096: 21, AR104: 21, AR089: 18, AR060: 15, AR061: 13 H0618: 8 and H0253: 4.	7q22	126650, 126650, 154276, 173360, 173360, 602136, 602136, 602136, 602447	43-59
152	HEQBJ81	725228	162	127 - 888	1567	Glu-122 to Lys-127, Glu-161 to Val-168, Thr-178 to Trp-189.	AR104: 4, AR033: 4, AR089: 3, AR053: 3, AR052: 3, AR096: 2, AR061: 2, AR060: 2, AR055: 2, AR039: 2 L0803: 6, L0771: 5, L0439: 5, L0769: 4, L0805: 4, L0759: 4, L0747: 3, L0777: 3, L0758: 3, H0156: 2, H0618: 2, H0052: 2, H0545: 2, L0163: 2, H0644: 2, S0440: 2, L0644: 2,	3p21.3	116806, 120120, 120120, 120120, 120436, 120436, 120436, 138320, 168468, 182280, 600163	221-238, 54-70

153	HAGES18	725655	163	215 - 568	1568	Met-1 to Lys-11, Gln-72 to Gly-77.	L0766: 2, L0653: 2, L0665: 2, H0539: 2, L0748: 2, L0731: 2, L0593: 2, H0624: 1, H0556: 1, T0002: 1, H0713: 1, H0650: 1, H0657: 1, H0402: 1, S0360: 1, S0132: 1, H0619: 1, L0717: 1, S0278: 1, H0642: 1, H0486: 1, T0039: 1, H0013: 1, H0253: 1, S0665: 1, H0544: 1, H0546: 1, H0009: 1, H0620: 1, H0014: 1, H0083: 1, S6028: 1, H0288: 1, H0674: 1, S0366: 1, H0591: 1, H0412: 1, H0100: 1, T0042: 1, L0475: 1, H0561: 1, H0647: 1, S0144: 1, H0529: 1, L0763: 1, L0772: 1, L0372: 1, L0662: 1, L0363: 1, L0794: 1, L0775: 1, L0776: 1, L0809: 1, L0666: 1, L0663: 1, H0702: 1, H0520: 1, S0126: 1, H0435: 1, H0658: 1, S0332: 1, H0478: 1, L0751: 1, L0750: 1, L0755: 1, L0592: 1, L0366: 1, H0542: 1, H0423: 1 and H0677: 1.	AR033: 28, AR060: 19, AR104: 19, AR089: 18,		22-63, 51-67

						AR096: 13, AR061: 8, AR055: 6, AR053: 5, AR052: 5, AR039: 3			69-85, 27-44, 112-128
154	HHSGV20	725822	164	183 - 575	1569	Arg-14 to Pro-20.	AR104: 21, AR033: 17, AR055: 11, AR060: 6, AR061: 6, AR039: 6, AR089: 6, AR053: 5, AR052: 4, AR096: 4 L0439: 13, H0052: 8, L0769: 5, L0755: 5, L0770: 4, L0754: 4, L0753: 4, L0758: 4, L0794: 3, L0775: 3, L0806: 3, L0776: 3, L0752: 3, S0360: 2, H0261: 2, S0388: 2, H0213: 2, L0804: 2, L0774: 2, L0807: 2, L0779: 2, L0603: 2, S0256: 1, H0255: 1, H0455: 1, H0009: 1, H0172: 1, S0051: 1, T0010: 1, T0006: 1, H0033: 1, H0424: 1, S0364: 1, S0036: 1, H0038: 1, H0131: 1, L0764: 1, L0803: 1, L0805: 1, L0809: 1, L0787: 1, L0790: 1, L0663: 1, H0521: 1, L0742: 1, L0751: 1, L0745: 1, L0731: 1 and L0485: 1.		

155	HNECD53	727386	165	117 - 554	1570	Pro-13 to Ser-19, Ala-21 to Asp-30, Gln-41 to Val-48, Asp-108 to Leu-113.	AR096: 4, AR055: 3, AR033: 3, AR060: 2, AR052: 2, AR089: 2, AR053: 2, AR061: 2, AR104: 0 L0731: 8, L0794: 7, L0803: 4, H0265: 3, L0809: 3, L0596: 3, L0766: 2, L0659: 2, L0565: 2, L0595: 2, H0556: 1, S0134: 1, H0657: 1, H0341: 1, S0356: 1, H0411: 1, S0222: 1, T0104: 1, H0013: 1, H0618: 1, H0597: 1, H0050: 1, H0620: 1, H0179: 1, H0292: 1, H0553: 1, T0067: 1, H0412: 1, S0422: 1, L0644: 1, L0662: 1, L0804: 1, L0805: 1, L0636: 1, L0789: 1, L0665: 1, S0126: 1, S0152: 1, H0704: 1, H0215: 1, L0786: 1, L0779: 1, L0777: 1, L0780: 1, L0758: 1, L0759: 1, L0608: 1 and L0361: 1.				121-144, 89-105
156	HRAAO53	728064	166	71 - 403	1571	Arg-7 to Leu-15.	AR052: 4, AR039: 3, AR104: 3, AR033: 2, AR096: 2, AR060: 2, AR053: 2, AR055: 2, AR089: 1, AR061: 1	13q14.1-q14.2	136533, 180200, 180200, 180200, 180200,		34-54, 83-101

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157	HDPGD34	728098	167	132 - 863	1572	Tyr-5 to Gly-13, Ala-23 to Leu-38, Tyr-82 to Leu-95, Asn-126 to Asp-146, Pro-153 to Pro-167.	1, H0667: 1, S0276: 1, S0424: 1, S0462: 1, S0456: 1, H0008: 1 and H0352: 1.	AR096: 1, AR104: 1, AR089: 1, AR060: 1, AR061: 0, AR033: 0, AR039: 0, AR052: 0, AR055: 0, AR053: 0 L0740: 10, H0521: 8, L0659: 7, L0666: 7, L0731: 7, L0664: 6, L0754: 6, L0803: 5, L0752: 5, S0003: 4, L0770: 4, L0771: 4, L0438: 4, H0547: 4, S0380: 4, S0152: 4, H0522: 4, L0755: 4, H0171: 3, S0212: 3, S0358: 3, H0013: 3, H0545: 3, H0623: 3, S0344: 3, H0520: 3, S0126: 3, H0648: 3, H0539: 3, L0602: 3, L0744: 3, L0750: 3, L0758: 3, L0599: 3, S0026: 3, S0192: 3, S0242: 3, L0005: 2, S0360: 2, H0581: 2, H0510: 2, H0375: 2, L0483: 2, H0169: 2, H0090: 2, H0379: 2, H0056: 2, H0560: 2, L0662: 2, L0794: 2, L0766: 2, L0775: 2, H0660: 2, L0757: 2, H0667:			40-72

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158	HLYBU12	728763	168	212 - 769	1573	Thr-35 to Lys-40, Pro-63 to Gln-69, Leu-122 to Thr-128.	AR096: 1, AR052: 1, AR104: 1, AR033: 1, AR089: 0, AR053: 0, AR055: 0, AR061: 0, AR060: 0 L0766: 5, L0748: 3, L0758: 3, L0791: 2, S0328: 2, L0747: 2, L0777: 2, H0251: 1, H0673: 1, L0803: 1, L0806: 1, L0665: 1, H0547: 1, H0436: 1, L0749: 1, L0756: 1, L0779: 1, L0759: 1, H0445: 1 and L0592: 1.			
159	HEONV59	728861	169	157 - 972	1574	Tyr-81 to Ile-88, Ala-113 to Gln-118, Asn-183 to Ser-189.	AR096: 2, AR055: 1, AR089: 1, AR033: 1, AR060: 1, AR061: 0, AR053: 0, AR039: 0, AR104: 0, AR052: 0 H0457: 1 and H0521: 1.			230-267, 2-18, 87-103
160	HCWHX54	728903	170	95 - 445	1575		AR061: 0, AR060: 0, AR096: 0, AR033: 0,			88-105, 60-76

161	HE8DF23	730794	171	739 - 1101	1576	Arg-26 to Gln-35, Arg-41 to Asn-46, Tyr-80 to Ser-85.	AR052: 0, AR039: 0, AR104: 0, AR089: 0, AR055: 0, AR053: 0 H0305: 1 and H0423: 1.			103-119, 55-71
							AR053: 19, AR052: 17, AR089: 12, AR096: 12, AR055: 12, AR060: 8, AR033: 7, AR061: 5, AR104: 4, AR039: 3 L0766: 4, L0779: 4, L0803: 3, L0747: 3, L0752: 3, H0039: 2, H0059: 2, L0794: 2, S0027: 2, L0744: 2, L0740: 2, L0777: 2, L0759: 2, S0430: 1, S0418: 1, S0358: 1, S6014: 1, H0497: 1, H0013: 1, H0575: 1, H0123: 1, H0510: 1, H0040: 1, L0761: 1, L0662: 1, L0804: 1, L0774: 1, L0775: 1, L0776: 1, L0384: 1, L0787: 1, L0663: 1, H0702: 1, H0547: 1, H0682: 1, H0696: 1, L0749: 1, L0753: 1, L0731: 1, H0445: 1, H0595: 1, S0276: 1 and H0542: 1.			
162	HOECO53	730924	172	113 - 439	1577	Phe-22 to Asn-33, Ala-68 to Gly-73.	AR039: 53, AR033: 27, AR096: 21, AR055: 20,			43-62, 1-17

							AR053: 19, AR104: 18, AR052: 18, AR089: 18, AR061: 15, AR060: 15 S0126: 10, L0766: 5, S0027: 5, L0748: 5, L0754: 5, H0484: 4, S0007: 4, H0370: 4, H0617: 4, H0087: 4, L0803: 4, L0776: 4, L0744: 4, L0758: 4, S0360: 3, S0408: 3, S0045: 3, S0046: 3, S0278: 3, H0544: 3, H0545: 3, H0023: 3, S0144: 3, S0142: 3, L0773: 3, L0794: 3, L0655: 3, L0659: 3, L0751: 3, L0747: 3, H0543: 3, H0422: 3, S0040: 2, H0295: 2, H0341: 2, S0029: 2, H0549: 2, H0441: 2, H0486: 2, H0069: 2, H0530: 2, H0150: 2, H0050: 2, H0057: 2, H0510: 2, H0424: 2, H0634: 2, H0551: 2, L0763: 2, L0646: 2, L0378: 2, L0806: 2, L0805: 2, H0539: 2, H0710: 2, H0696: 2, S3014: 2, S0028: 2, L0742: 2, L0745: 2, L0750: 2, L0755: 2, L0757: 2, H0445: 2, S0436: 2, H0542: 2, H0423: 2,			

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163	HDFAB91	731889	173	375 - 1022	1578	Cys-30 to Tyr-36, Thr-41 to Gly-46, Val-111 to His-122, Pro-201 to Arg-206, Pro-209 to His-216.	AR033: 7, AR052: 2, AR089: 1, AR053: 1, AR061: 1, AR060: 1, AR055: 0, AR096: 0, AR104: 0, AR039: 0 L0769: 8, L0794: 8, L0439: 7, H0399: 3, L5565: 3, L0758: 3, H0253: 2, H0051: 2, L0438: 2, L0748: 2, L0777: 2, H0624: 1, H0441: 1, H0438: 1, L0021: 1, H0618: 1, S0049: 1, H0562: 1, S0050: 1, S0051: 1, L0638: 1, L0789: 1, H0547: 1, H0658: 1, L0743: 1, L0753: 1, S0031: 1 and S0260: 1.			
164	HWLER32	732236	174	157 - 666	1579	Lys-45 to Arg-52.	AR096: 75, AR089: 75, AR039: 63, AR104: 56, AR053: 46, AR052: 36,			5-26, 90-108, 52-72

						AR060: 31, AR033: 30, AR055: 11, AR061: 10 L0748: 3, S0354: 1, H0421: 1, H0355: 1, S0428: 1 and S0031: 1.			43-59
165	HNFJE71	732600	175	29 - 430	1580	Gln-2 to Lys-7, Glu-35 to Thr-42, Arg-64 to Ser-72.	AR055: 9, AR052: 7, AR060: 4, AR033: 4, AR061: 4, AR089: 3, AR096: 3, AR053: 3, AR039: 1, AR104: 1 H0271: 11, L0759: 4, L0779: 3, L0755: 3, H0222: 2, H0575: 2, H0705: 2, H0581: 2, H0622: 2, H0030: 2, L0803: 2, L0659: 2, L0790: 2, L0754: 2, L0749: 2, L0777: 2, L0591: 2, H0556: 1, H0159: 1, T0049: 1, H0650: 1, S0418: 1, S0045: 1, H0437: 1, T0060: 1, H0069: 1, H0599: 1, H0046: 1, L0163: 1, S0051: 1, H0083: 1, H0179: 1, H0416: 1, H0039: 1, H0553: 1, H0628: 1, S0366: 1, H0038: 1, H0551: 1, H0488: 1, H0268: 1, H0059: 1, T0042: 1, S0422: 1, H0529: 1, L0770: 1, L0667: 1, L0800: 1, L0641: 1, L0773:			

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166	HOUHA56	732902	176	114 - 536	1581	Phe-6 to Ser-16.	AR033: 6, AR104: 2, AR060: 1, AR052: 1, AR089: 1, AR061: 0, AR055: 0, AR039: 0, AR096: 0, AR053: 0 S0342: 1				
167	HMSHT01	733800	177	664 - 248	1582	Phe-70 to Val-76.	AR060: 6, AR033: 6, AR055: 6, AR089: 5, AR096: 5, AR104: 5, AR052: 3, AR053: 3, AR061: 3, AR039: 1 H0399: 4, L0805: 3, H0661: 2, S0356: 2, H0457: 2, L0794: 2, L0775: 2, L0663: 2, L0747: 2, L0759: 2, L0005: 1, H0580: 1, S0222: 1, H0156: 1, L0021: 1, H0575: 1, H0581: 1, H0327: 1, H0123: 1, H0012: 1, H0057: 1, S0051: 1, H0328: 1, H0163: 1, H0038: 1, H0413: 1, H0100: 1,			86-103, 30-46

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168	HAPQM57	734582	178	96 - 401	1583	Arg-16 to Glu-27.		AR055: 9, AR061: 8, AR033: 6, AR052: 6, AR060: 5, AR089: 4, AR053: 4, AR096: 2, AR039: 1, AR104: 1 H0351: 2, H0575: 2, L0794: 2, L0803: 2, L0751: 2, H0333: 1, H0390: 1, H0553: 1, L0645: 1, L0766: 1, L0439: 1, L0747: 1, L0749: 1 and L0601: 1.			194-211, 73-89
169	HSLJK58	735584	179	233 - 880	1584	Pro-5 to Thr-10, Lys-23 to Asn-33, Gln-105 to Tyr-115.		AR055: 4, AR033: 3, AR096: 3, AR052: 3, AR061: 3, AR039: 2, AR060: 2, AR089: 2, AR053: 1, AR104: 1 L0783: 2, L0751: 2, H0409: 1, H0559: 1, L0471: 1, H0646: 1, H0658: 1, S0390: 1, L0777: 1, L0731: 1 and L0462: 1.			
170	HSLHL67	735747	180	35 - 673	1585	Glu-40 to Tyr-45.		AR096: 8, AR053: 7,			62-78, 20-

						AR060: 7, AR039: 6, AR089: 6, AR052: 6, AR055: 6, AR104: 5, AR033: 5, AR061: 4 S0280: 1, H0488: 1, H0509: 1 and S0028: 1.			36, 111-127	
171	HCEMF51	738228	181	681 - 1148	1586	Arg-11 to Ser-24, Ser-37 to Ala-43.	AR055: 10, AR060: 7, AR033: 6, AR061: 6, AR089: 6, AR052: 4, AR053: 4, AR096: 4, AR104: 3, AR039: 2 H0052: 5, L0748: 5, L0756: 4, L0731: 4, S0360: 3, L0764: 3, L0747: 3, L0749: 3, H0255: 2, H0333: 2, L0055: 2, L0653: 2, L0740: 2, L0754: 2, L0750: 2, L0596: 2, H0352: 2, H0556: 1, H0341: 1, H0662: 1, H0306: 1, H0402: 1, H0036: 1, H0434: 1, H0150: 1, L0456: 1, H0135: 1, H0413: 1, H0059: 1, H0529: 1, L0770: 1, L0769: 1, L0630: 1, L0521: 1, L0662: 1, L0775: 1, L0776: 1, L0493: 1, H0684: 1, S0328: 1, S0044: 1, L0777: 1, L0752: 1, L0755: 1, L0758: 1 and S0242: 1.			98-116, 136-152	

172	HTHCV59	738569	182	59 - 373	1587		AR089: 17, AR060: 15, AR096: 15, AR055: 13, AR039: 13, AR033: 12, AR104: 11, AR052: 10, AR053: 8, AR061: 7 H0318: 1 and H0063: 1.			83-102, 10-26
173	HCHCI12	738911	183	129 - 656	1588	Ser-22 to His-33, Pro-85 to Asn-94, Phe-101 to Gln-108.	AR061: 3, AR052: 2, AR089: 2, AR055: 2, AR033: 2, AR104: 2, AR096: 2, AR060: 1, AR053: 1, AR039: 0 L0742: 4, H0484: 2, L0763: 2, L0758: 2, H0483: 1, H0618: 1, H0047: 1, H0188: 1, S0344: 1, L0637: 1, L0771: 1, L0803: 1, L0628: 1, H0683: 1, H0522: 1 and L0752: 1.			48-64, 121-137
174	HOEAU34	739003	184	149 - 526	1589	Ala-9 to Leu-16.	AR089: 9, AR060: 8, AR033: 7, AR096: 2, AR053: 1, AR061: 1, AR055: 0, AR052: 0, AR039: 0, AR104: 0 L0809: 3, H0442: 2, S0010: 2, L0794: 2, L0803: 2, S0378: 2, H0341: 1, S0376: 1, H0611: 1, H0486: 1, H0013: 1, H0156: 1, L0021: 1, H0318: 1, H0123:			47-67

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175	HFASN59	739048	185	45 - 368	1590		AR104: 1, AR061: 1, AR060: 0, AR039: 0, AR033: 0, AR089: 0 L0794: 3, L0749: 2, L0731: 2, H0650: 1, S0408: 1, S0300: 1, L0456: 1, L0769: 1, L0637: 1, L0643: 1, L0650: 1, L0659: 1, L0792: 1, L0666: 1, L0438: 1, H0696: 1 and L0747: 1.			
176	HLHCU82	739503	186	152 - 490	1591	Lys-5 to Glu-11, Tyr-17 to Asp-25.	AR055: 6, AR096: 5, AR052: 5, AR060: 4, AR089: 4, AR061: 4, AR053: 4, AR033: 3, AR104: 1, AR039: 0 L0362: 20, L0766: 11, L0754: 10, L0747: 5, L0731: 4, S0003: 3, H0547: 3, S0026: 3, S0212: 2, H0251: 2, H0046: 2, H0031:	11q13.5	133780, 266150, 276903, 276903, 276903	61-78

177	HSDJN50	740786	187	2615 - 2247	1592	Ala-87 to Ala-97.	2, H0674: 2, L0769: 2, L0663: 2, L0665: 2, H0144: 2, L0438: 2, L0748: 2, L0439: 2, H0445: 2, H0170: 1, H0686: 1, T0049: 1, S0134: 1, H0657: 1, S0001: 1, H0459: 1, S0360: 1, S0410: 1, S0468: 1, H0431: 1, H0497: 1, H0486: 1, S0280: 1, H0196: 1, H0596: 1, H0565: 1, H0571: 1, H0566: 1, H0024: 1, H0275: 1, H0267: 1, S0214: 1, H0615: 1, H0090: 1, H0040: 1, H0634: 1, H0413: 1, S0440: 1, S0208: 1, H0529: 1, L0640: 1, L0770: 1, L0642: 1, L0794: 1, L0649: 1, L0803: 1, L0804: 1, L0650: 1, L0774: 1, L0775: 1, L0805: 1, L0661: 1, L0783: 1, L0809: 1, L0666: 1, L0664: 1, H0519: 1, H0684: 1, H0672: 1, S0406: 1, L0740: 1, L0750: 1, L0779: 1, L0758: 1, S0434: 1, L0589: 1, S0106: 1, H0667: 1 and S0424: 1.	AR096: 9, AR053: 9, AR052: 7, AR089: 6,		46-68, 21-42, 66-82,

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					Ser-23 to Lys-37, Thr-61 to Pro-66.	AR052: 11, AR053: 9, AR033: 7, AR096: 7, AR104: 6, AR089: 6, AR060: 4, AR055: 3, AR061: 2, AR039: 2 S0354: 5, S0426: 5, S0002: 3, S0278: 2, L0375: 2, L0751: 2, L0758: 2, L0539: 1, H0392: 1, H0592: 1, H0318: 1, L0041: 1, H0494: 1, S0144: 1, S0142: 1, S0344: 1, L0803: 1, L0804: 1, L0805: 1, L0776: 1, S0052: 1, S0428: 1, S0053: 1, H0144: 1, S0378: 1,		89-106, 40-56
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179	HKAAA18	741128	189	139 - 555	1594	Lys-5 to Glu-11, Tyr-17 to Asp-25, Lys-39 to Ile-45, Val-81 to Leu-93, Thr-100 to Phe-106, Thr-117 to Glu-126, Thr-128 to Gln-133.	AR053: 24, AR052: 19, AR096: 7, AR089: 3, AR033: 2, AR039: 2, AR104: 2, AR060: 2, AR055: 1, AR061: 1 H0486: 1 and H0494: 1.	11q13.5	133780, 266150, 276903, 276903, 276903	61-78
180	HISCL61	741659	190	19 - 483	1595	Leu-44 to Glu-49, Tyr-61 to Cys-68, Glu-94 to Ile-108.	AR096: 2, AR060: 1, AR089: 1, AR104: 1, AR033: 1, AR055: 0, AR061: 0, AR052: 0, AR039: 0, AR053: 0 L0766: 2, L0776: 2, L0759: 2, T0002: 1, H0329: 1, H0604: 1, H0424: 1, S0144: 1, L0800: 1, L0644: 1, L0662: 1, L0804: 1, L0775: 1, L0806: 1, L0805: 1, L0659: 1, H0593: 1, H0539: 1, H0521: 1, L0786: 1, L0731: 1 and L0601: 1.	19		73-89, 109-125
181	HAGDA61	741921	191	112 - 492	1596	Pro-6 to Thr-21, Asp-47 to Ile-57, Lys-76 to Tyr-90.	AR104: 74, AR096: 39, AR089: 34, AR039: 33, AR033: 24, AR052: 23, AR060: 23, AR053: 20, AR055: 11, AR061: 6 S0010: 1, L0740: 1 and L0752: 1.			99-119

182	HFIIO11	742518	192	535 - 209	1597	Met-1 to Gly-7, Ala-16 to Gln-21, Ser-35 to Gly-41, Thr-43 to Asn-52.	AR096: 5, AR089: 3, AR060: 3, AR033: 2, AR104: 2, AR052: 1, AR039: 1, AR053: 1, AR055: 1, AR061: 1 H0038: 3, L0439: 3, H0039: 2, L0740: 2, L0747: 2, L0756: 2, H0592: 1, H0318: 1, H0031: 1, H0644: 1, L0766: 1, L0774: 1, L0666: 1, L0438: 1, L0754: 1, L0779: 1, L0758: 1, S0192: 1, S0194: 1 and H0506: 1.			62-78, 92-108
183	HUSGB32	742690	193	46 - 840	1598	Glu-4 to Gly-12, Gly-19 to Ser-37, Gln-49 to Asn-54, Glu-102 to Cys-108, Leu-116 to Asn-125.	AR033: 9, AR089: 4, AR052: 3, AR096: 3, AR053: 3, AR055: 3, AR060: 3, AR104: 2, AR061: 1, AR039: 1 L0748: 2, H0581: 1, H0046: 1, L0483: 1, H0634: 1, H0412: 1, S0150: 1, H0520: 1, L0612: 1 and H0543: 1.			54-71, 133-149
184	HTXED15	743383	194	101 - 442	1599	Ser-43 to Val-53.	AR033: 7, AR060: 5, AR089: 5, AR061: 2, AR039: 2, AR096: 1, AR055: 0, AR053: 0, AR052: 0			55-71, 24-40, 74-90

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185	HCFMF12	743426	195	25 - 333	1600		AR052: 3, AR089: 2, AR033: 2, AR053: 2, AR060: 2, AR055: 1, AR096: 1, AR104: 1, AR061: 1, AR039: 0 H0521: 2, H0305: 1, H0046: 1, S0144: 1, S0002: 1, H0478: 1, L0748: 1, H0543: 1, H0423: 1 and H0422: 1.			75-91
186	HSSJG62	744278	196	55 - 573	1601		AR055: 20, AR039: 13, AR052: 13, AR053: 11, AR061: 11, AR096: 10, AR033: 10, AR089: 9, AR060: 9, AR104: 7 H0428: 2, H0135: 2, L0794: 2, L0779: 2, L0770: 1, L0766: 1, L0774: 1, L0789: 1, L0792: 1, L0439: 1, L0731: 1 and L0757: 1.	19p12	601843	128-146, 21-37, 63-79
187	HFIHF63	744330	197	201 - 611	1602	Gly-14 to Gly-23.	AR053: 1, AR096: 1, AR055: 1, AR052: 1, AR089: 1, AR033: 1, AR061: 1, AR060: 1, AR104: 0, AR039: 0 L0747: 5, L0809: 3,	19p13.3	108725, 120700, 133171, 136836, 145981, 147141,	96-124

188	HMDAG54	744453	198	759 - 1223	1603	Tyr-9 to Asn-15, Arg-57 to Trp-64, Pro-68 to Ala-78, Gln-83 to Asp-88, Pro-106 to Ser-112.	L0731: 3, L0759: 3, L0777: 2, L0752: 2, L0021: 1, S0250: 1, H0252: 1, L0770: 1, L0774: 1, L0792: 1, L0793: 1, L0750: 1, L0779: 1, L0758: 1 and S0194: 1.	AR033: 1, AR089: 0, AR061: 0, AR096: 0, AR060: 0, AR053: 0, AR104: 0, AR052: 0, AR055: 0, AR039: 0 L0372: 2, L0748: 2, L0439: 2, L0751: 2, L0754: 2, L0750: 2, L0756: 2, L0779: 2, L0755: 2, H0170: 1, S0212: 1, S0282: 1, H0346: 1, S0376: 1, S0360: 1, T0040: 1, H0253: 1, H0424: 1, H0553: 1, H0674: 1, L0772: 1, L0764: 1, L0771: 1, L0803: 1, L0776: 1, L0659: 1, H0144: 1, S0374: 1 and L0747: 1.	164953, 188070, 600957, 601238, 601846, 602216, 602477	115-131
189	HCHMI51	744616	199	234 - 584	1604			AR096: 1, AR089: 1, AR033: 1, AR039: 0, AR061: 0, AR053: 0, AR104: 0, AR060: 0, AR052: 0, AR055: 0		71-99, 22-50

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190	HAHEA63	744726	200	220 - 531	1605		AR033: 38, AR089: 32, AR052: 29, AR104: 27, AR096: 27, AR060: 22, AR053: 22, AR055: 11, AR039: 11, AR061: 9 H0599: 5, H0575: 3, L0438: 2, S0212: 1, S0420: 1, S0356: 1, H0393: 1, H0549: 1, H0391: 1, H0036: 1, T0071: 1, H0581: 1, S0051: 1, H0266: 1, H0271: 1, H0292: 1, H0272: 1, L0435: 1, H0280: 1, H0561: 1, H0509: 1, L0762: 1, H0547: 1, H0435: 1, H0521: 1, S0028: 1, L0439: 1, H0542: 1, H0543: 1 and H0423: 1.			
191	HAJAN63	744831	201	108 - 500	1606	Ser-21 to Trp-28, Arg-63 to Val-68.	AR039: 12, AR096: 7, AR104: 7, AR033: 6,			76-107, 1-17, 114-

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193	HCHOH38	746390	203	140 - 904	1608	Gly-7 to Lys-16, Gly-84 to Pro-90, Pro-100 to Ser-106.	AR104: 10, AR033: 7, AR096: 5, AR089: 4, AR052: 3, AR053: 3, AR039: 3, AR060: 3, AR055: 1, AR061: 1 S0001: 4, L0439: 4, H0617: 3, L0776: 3, L0438: 3, L0748: 3, H0484: 2, S0420: 2, S0222: 2, H0274: 2, H0181: 2, H0529: 2, L0517: 2, L0789: 2, H0659: 2, L0751: 2, L0596: 2, L0361: 2, H0295: 1, T0049: 1, H0656: 1, S0418: 1, L0005: 1, S0476: 1, H0645: 1, H0333: 1, L0021: 1, H0036: 1, H0052: 1, H0597: 1, H0545: 1, H0009: 1, H0178: 1, H0081: 1, S0388: 1, H0673: 1, S0036: 1, H0038: 1, H0494: 1, L0769: 1, L0796: 1, L0372: 1, L0800: 1, L0643: 1, L0645: 1, L0521: 1, L0768: 1, L0364: 1, L0803: 1, L0806: 1, L0805: 1, L0792: 1, L0807: 1, L0809: 1, L0666: 1, H0144: 1, H0547: 1, L0749: 1, L0779: 1 and L0758: 1.			177-195, 53-69, 150-166, 16-32

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194	HMSBS61	746583	204	783 - 1	1609	Thr-17 to Glu-25, Glu-61 to Val-66, Leu-122 to Cys-129, Glu-139 to Asp-148, Pro-169 to Val-179, Lys-183 to Gly-193.	AR052: 11, AR053: 10, AR096: 9, AR055: 7, AR033: 6, AR060: 5, AR039: 5, AR061: 4, AR089: 4, AR104: 4 L0748: 14, H0457: 9, L0766: 8, H0543: 7, L0731: 6, L0439: 5, L0770: 4, L0747: 4, H0542: 4, S0002: 3, L0777: 3, H0445: 3, S0434: 3, S0192: 3, H0423: 3, S0114: 2, H0575: 2, S0010: 2, L0667: 2, L0646: 2, L0775: 2, L0655: 2, H0436: 2, L0749: 2, L0594: 2, H0422: 2, S0342: 1, S0134: 1, H0583: 1, S0212: 1, S0376: 1, S0045: 1, S0046: 1, S0476: 1, S0222: 1, H0486: 1, H0635: 1, H0156: 1, S0346: 1, S0474: 1, H0263: 1, H0572: 1,			

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196	HTPCT63	747208	206	53 - 556	1611	Tyr-14 to Glu-19, Lys-48 to Asp-91.	AR053: 21, AR052: 15, AR096: 13, AR089: 12, AR060: 10, AR055: 9, AR033: 9, AR104: 7, AR061: 6, AR039: 6 H0486: 2, L0747: 2, S0298: 1, H0392: 1, T0010: 1, H0039: 1, H0529: 1, L0766: 1, L0438: 1, L0731: 1, L0591: 1 and H0543: 1.			106-122
197	HE8NL29	750243	207	470 - 72	1612		AR089: 1, AR096: 0, AR060: 0, AR052: 0, AR104: 0, AR061: 0, AR053: 0, AR033: 0, AR039: 0 H0013: 2 and S0218: 1.			109-125, 6-22
198	HTTFM66	750750	208	117 - 434	1613		AR055: 8, AR053: 6, AR052: 6, AR060: 5, AR096: 4, AR061: 4, AR033: 4, AR039: 3, AR089: 3, AR104: 3 H0040: 2			62-96, 17-48, 89-105
199	HE9EM20	751048	209	2 - 751	1614	Cys-175 to Val-181, Lys-184 to Arg-204, Gln-218 to Glu-227, Lys-233 to Phe-242.	AR055: 12, AR060: 12, AR061: 9, AR033: 8, AR104: 8, AR096: 7, AR089: 6, AR053: 5, AR052: 4, AR039: 4			112-128, 56-72

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							1, H0574: 1, H0575: 1, H0590: 1, L0040: 1, H0051: 1, H0169: 1, H0674: 1, H0412: 1, L0645: 1, L0767: 1, L0666: 1, L0665: 1, H0547: 1, H0539: 1, H0478: 1, L0611: 1, L0741: 1, L0750: 1 and S0434: 1.			
201	HTGAU79	751677	211	203 - 961	1616	Ala-10 to Glu-18, Arg-26 to Arg-31, Phe-48 to Gln-53, Gly-77 to Glu-84, Met-130 to Gly-138, Tyr-225 to Ala-232.	AR055: 8, AR053: 6, AR052: 6, AR033: 6, AR060: 5, AR089: 5, AR096: 4, AR061: 4, AR039: 3, AR104: 3 H0551: 3, H0529: 3, L0770: 3, L0769: 3, L0794: 3, L0758: 3, S0418: 2, L0773: 2, L0521: 2, H0701: 2, S0126: 2, L0747: 2, L0731: 2, L0759: 2, L0589: 2, L0601: 2, H0624: 1, H0149: 1, H0556: 1, H0295: 1, S0134: 1, H0583: 1, H0661: 1, S0476: 1, H0592: 1, H0013: 1, H0635: 1, H0581: 1, S0250: 1, H0212: 1, H0412: 1, S0438: 1, S0440: 1, S0144: 1, L0763: 1, L0645: 1, L0764: 1, L0766: 1, L0775: 1, L0783: 1, L0665: 1, H0519: 1,			175-192, 94-110

							H0435: 1, H0672: 1, H0436: 1, S3014: 1, S0028: 1, L0750: 1, L0777: 1, S0436: 1, L0366: 1, H0667: 1 and H0423: 1.			69-103, 90-106, 1-17
202	HETAJ12	751735	212	17 - 463	1617	Pro-26 to Pro-31, Pro-119 to Asp-124, Gln-132 to Leu-140, Arg-143 to Pro-149.	AR055: 3, AR033: 2, AR104: 2, AR060: 2, AR053: 2, AR039: 2, AR089: 1, AR061: 1, AR096: 1, AR052: 0 H0046: 2, H0431: 1, S0428: 1 and H0660: 1.			
203	HDABX16	752630	213	64 - 456	1618		AR096: 8, AR052: 7, AR039: 6, AR053: 6, AR033: 5, AR089: 4, AR055: 4, AR104: 3, AR061: 3, AR060: 3 H0618: 9, L0751: 7, L0754: 6, L0758: 6, H0253: 5, L0748: 5, L0439: 5, H0580: 3, H0052: 3, L0770: 3, L0663: 3, H0556: 2, S0418: 2, H0733: 2, H0351: 2, H0706: 2, H0567: 2, H0625: 2, S0144: 2, S0142: 2, L0659: 2, L0543: 2, L5623: 2, L0749: 2, S0436: 2, H0423: 2, H0381: 1, S0212: 1, H0254: 1, H0663:			57-76, 114-130

204	HFEBM11	753105	214	27 - 458	1619	Asp-20 to Glu-26,	AR033: 12, AR055: 11, 1, H0638: 1, S0045: 1, S0046: 1, S0476: 1, S6022: 1, H0549: 1, H0550: 1, S0222: 1, H0370: 1, H0497: 1, H0574: 1, L0622: 1, L0623: 1, H0101: 1, H0427: 1, S0280: 1, H0122: 1, H0194: 1, H0596: 1, H0570: 1, H0081: 1, H0620: 1, H0014: 1, H0083: 1, H0355: 1, H0510: 1, H0424: 1, H0030: 1, H0553: 1, H0628: 1, S0364: 1, S0366: 1, H0038: 1, H0551: 1, H0100: 1, L0351: 1, H0494: 1, S0438: 1, H0633: 1, S0422: 1, L0371: 1, L0769: 1, L0639: 1, L0772: 1, L0648: 1, L0497: 1, L0375: 1, L0511: 1, L0666: 1, H0144: 1, H0520: 1, H0593: 1, H0682: 1, H0670: 1, H0672: 1, H0539: 1, H0521: 1, S0044: 1, H0555: 1, H0626: 1, H0732: 1, S3012: 1, S3014: 1, S0027: 1, S0028: 1, L0779: 1, L0584: 1, L0608: 1, L0593: 1, H0667: 1 and H0542: 1.	5q31.1	131400,	110-136

						Asp-48 to Tyr-57, Asn-59 to Gly-66, Ala-69 to Gly-76, Ser-91 to Asn-97.	AR089: 10, AR052: 9, AR061: 9, AR053: 8, AR060: 8, AR096: 4, AR039: 3, AR104: 0 H0081: 1, H0509: 1 and S0330: 1.		147061, 147575, 147575, 147575, 153455, 159000, 181460, 600807, 601596, 602089	
205	HHGBS74	753235	215	979 - 1584	1620	Ser-26 to Asn-35, Gly-95 to Pro-100, Arg-115 to Gln-126, Arg-132 to Asp-137, Val-183 to Ser-188.	AR052: 297, AR053: 285, AR096: 212, AR039: 173, AR089: 146, AR055: 106, AR104: 92, AR060: 90, AR061: 69, AR033: 67 H0169: 4, L0529: 2, H0624: 1, H0341: 1, H0333: 1, H0013: 1, H0266: 1, H0674: 1, H0269: 1, S0440: 1, L0770: 1, L0809: 1, L0780: 1 and L0758: 1.			76-93, 38-54
206	HTAAT39	753289	216	456 - 959	1621	Ser-50 to Thr-55, Ser-67 to Asp-72, Ala-105 to Ser-110, Gln-139 to Lys-149, Arg-152 to Ser-166.	AR104:1068, AR061: 633, AR060: 627, AR055: 507, AR033: 469, AR089: 444, AR052: 279, AR039: 276, AR096: 237, AR053: 231 H0069: 5 and H0634: 1.			108-139
207	HHSFO30	754184	217	9 - 317	1622	Gly-15 to His-27, Pro-35 to Ser-44.	AR104: 18, AR033: 16, AR055: 9, AR060: 7,			46-63

							AR061: 7, AR052: 6, AR089: 6, AR053: 4, AR096: 4, AR039: 4 L0471: 1, S0388: 1, H0633: 1 and L0591: 1.			
208	HTAFE69	754529	218	34 - 366	1623	Lys-11 to Glu-29.	AR061: 6, AR096: 6, AR060: 6, AR089: 6, AR039: 6, AR033: 5, AR052: 5, AR055: 5, AR053: 4, AR104: 4 H0069: 3, L0794: 1, L0803: 1 and L0758: 1.			55-74, 88-104
209	HMSCM47	756579	219	218 - 1390	1624	Asp-44 to His-54, Gly-92 to Lys-98, Gln-110 to Gly-115, Tyr-135 to Gly-140, Gly-162 to Ala-167.	AR053: 11, AR096: 9, AR052: 8, AR089: 6, AR104: 6, AR060: 5, AR055: 4, AR039: 4, AR033: 4, AR061: 3 H0521: 2, H0170: 1, S0134: 1, H0662: 1, S0354: 1, H0580: 1, H0619: 1, S0278: 1, H0574: 1, H0599: 1, H0590: 1, H0596: 1, L0471: 1, H0024: 1, H0014: 1, L0163: 1, H0644: 1, H0551: 1, S0002: 1, H0658: 1, L0602: 1, H0522: 1, S3014: 1, L0731: 1, L0601: 1 and L0366: 1.			324-340, 235-251, 64-80, 344-360
210	HETLM70	756676	220	337 -	1625		AR055: 10, AR089: 8,			100-130,

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			1080				AR033: 8, AR053: 8, AR052: 7, AR061: 7, AR060: 5, AR039: 5, AR096: 4, AR104: 3 L0803: 3, S0406: 3, H0356: 2, L0800: 2, L0517: 2, L0666: 2, L0751: 2, L0779: 2, S0434: 2, L0601: 2, H0661: 1, S0442: 1, S0358: 1, S0444: 1, H0046: 1, H0150: 1, H0188: 1, H0617: 1, H0383: 1, H0673: 1, H0674: 1, L0662: 1, L0774: 1, L0775: 1, L0805: 1, L0657: 1, L0809: 1, L0544: 1, L0793: 1, L0665: 1, H0689: 1, H0683: 1, H0658: 1, H0648: 1, S0328: 1, S0330: 1, S0380: 1, H0696: 1, S0146: 1, L0754: 1, L0752: 1 and H0506: 1.			111-129, 95-111
211	HLYEN32	756950	221	21 - 407	1626	Leu-64 to Ala-75.	AR089: 5, AR052: 5, AR033: 4, AR053: 4, AR096: 3, AR061: 3, AR104: 2, AR060: 2, AR055: 2, AR039: 2 H0556: 4, H0169: 3, L0766: 3, L0742: 3, L0747: 3, S0360: 2, S0046: 2, H0587: 2, L0483: 2, T0006:				

212	HHFHU45	757207	222	234 - 659	1627	Gly-9 to Leu-25.	2, H0488: 2, H0059: 2, L0646: 2, S0404: 2, L0748: 2, L0439: 2, L0751: 2, H0542: 2, H0265: 1, S0040: 1, H0341: 1, S0444: 1, S0045: 1, S0132: 1, S0222: 1, H0438: 1, S0280: 1, H0599: 1, S0346: 1, H0052: 1, H0014: 1, L0163: 1, H0083: 1, H0687: 1, S0250: 1, H0328: 1, H0039: 1, L0455: 1, H0040: 1, H0551: 1, H0623: 1, H0633: 1, H0647: 1, S0002: 1, L0761: 1, L0771: 1, L0662: 1, L0659: 1, L0787: 1, L0793: 1, L0666: 1, L0664: 1, L0665: 1, H0144: 1, H0701: 1, H0520: 1, H0519: 1, S0126: 1, H0682: 1, H0672: 1, H0539: 1, S0380: 1, H0518: 1, H0696: 1, H0436: 1, S0028: 1, L0754: 1, L0750: 1, L0756: 1, L0752: 1, L0757: 1, L0758: 1, L0759: 1, H0445: 1, S0436: 1 and H0543: 1.	AR033: 2, AR089: 2, AR061: 1, AR060: 1, AR096: 0, AR039: 0,		83-99, 111-127

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						AR053: 0, AR055: 0 L0794: 6, L0758: 6, L0805: 4, L0748: 4, L0731: 4, L0806: 3, L0809: 3, L0750: 3, L0752: 3, L0759: 3, H0484: 2, H0486: 2, H0457: 2, H0150: 2, L0471: 2, H0620: 2, H0181: 2, S0002: 2, L0517: 2, L0666: 2, L0757: 2, S0116: 1, S0476: 1, S0278: 1, H0549: 1, H0013: 1, L0738: 1, H0050: 1, H0012: 1, H0622: 1, H0087: 1, T0067: 1, S0344: 1, L0763: 1, L0769: 1, L0800: 1, L0768: 1, L0803: 1, L0650: 1, L0775: 1, L0776: 1, L0655: 1, L0657: 1, L0658: 1, L0636: 1, L0384: 1, H0144: 1, S0374: 1, H0547: 1, H0696: 1, L0439: 1, L0751: 1, L0754: 1 and L0753: 1.			
					1628			
				311 - 631				
			223					
		757351						
	HHFHR59							
213						AR053: 9, AR055: 6, AR089: 5, AR060: 4, AR052: 4, AR096: 4, AR033: 4, AR061: 4, AR104: 0 H0050: 2, H0717: 1, S0420: 1, S0442: 1, H0253:		

							1, H0052: 1, H0135: 1, H0063: 1, H0494: 1, L0794: 1, L0649: 1, S0037: 1, L0439: 1, L0747: 1, S0434: 1 and H0506: 1.			156-172, 186-204, 85-101
214	HDPPA45	757472	224	148 - 891	1629	Ser-63 to Glu-72, Asn-123 to Thr-130, Pro-209 to Pro-215.	AR061: 1, AR096: 1, AR053: 0, AR089: 0, AR033: 0, AR055: 0, AR039: 0, AR060: 0, AR052: 0, AR104: 0 H0031: 3, L0800: 3, L0794: 3, L0666: 2, L0751: 2, H0265: 1, S0376: 1, H0559: 1, H0486: 1, H0156: 1, L0021: 1, H0599: 1, S0049: 1, H0545: 1, H0213: 1, H0059: 1, L0761: 1, L0649: 1, L0803: 1, L0655: 1, L4507: 1, H0723: 1, H0593: 1, H0539: 1, H0522: 1, L0756: 1, L0779: 1, L0755: 1, L0096: 1 and H0506: 1.			
215	HMAGC74	757601	225	87 - 437	1630		AR053: 9, AR052: 8, AR089: 6, AR055: 5, AR033: 5, AR096: 4, AR060: 3, AR061: 3, AR039: 2, AR104: 1 H0638: 5, L0761: 4,			59-76, 26-42

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216	HHFFR79	759851	226	37 - 813	1631	Ser-51 to Phe-57.	AR053: 4, AR052: 4, AR055: 4, AR096: 3, AR089: 3, AR033: 3, AR060: 3, AR061: 2, AR104: 2, AR039: 0 H0657: 2, H0485: 2, L0163: 2, H0356: 2, H0488: 2, L0763: 2, L0637: 2, L0646: 2, L0766: 2, L0754: 2, L0756: 2, L0591: 2, T0002: 1, H0497: 1, H0036: 1, H0590: 1, H0050: 1, H0071: 1, H0266: 1, S0003: 1, H0644: 1, L0142: 1, H0628: 1, S0438: 1, H0509: 1, S0422: 1, L0662: 1, L0794: 1, L0655: 1, L0657: 1, L0382: 1, L0665: 1, H0682: 1, H0659: 1, S0378: 1, S0146: 1, S0406: 1, L0779: 1, L0596: 1, S0106: 1, S0011: 1, S0242: 1, H0543: 1 and S0424: 1.			238-254
217	HMGBP83	759888	227	162 - 1289	1632	Lys-7 to Pro-14.	AR055: 6, AR060: 4, AR061: 3, AR089: 3, AR033: 3, AR052: 2, AR053: 2, AR096: 2, AR104: 2, AR039: 1 S0376: 1, H0580: 1, H0614: 1, H0284: 1, H0268:				259-293, 138-159, 36-57, 102-127, 235-252, 70-86, 325-341

							1, H0412: 1, H0623: 1, T0042: 1, S0126: 1, H0539: 1, H0521: 1 and L0779: 1.			
218	HAUBV24	760121	228	179 - 574	1633	Phe-60 to Gly-67.	AR061: 6, AR055: 4, AR060: 3, AR033: 3, AR039: 3, AR052: 3, AR089: 3, AR096: 2, AR053: 1, AR104: 1 L0749: 5, L0752: 5, L0748: 4, H0510: 2, S0440: 2, L0800: 2, S0436: 2, H0294: 1, H0393: 1, L0803: 1, L0774: 1, L0383: 1, L0789: 1 and L0779: 1.			7-37, 31-51, 67-90, 105-121
219	HWBAQ71	760146	229	90 - 392	1634		AR039: 6, AR053: 4, AR089: 3, AR104: 3, AR096: 3, AR052: 3, AR033: 2, AR055: 2, AR060: 2, AR061: 2 H0580: 1 and L0601: 1.			72-101, 32-53
220	HRACE71	760240	230	146 - 457	1635		AR039: 25, AR096: 18, AR089: 18, AR053: 12, AR060: 11, AR104: 11, AR052: 10, AR033: 10, AR055: 6, AR061: 3 S0050: 1 and H0555: 1.			57-73, 4-20
221	HADGC71	760321	231	20 - 460	1636	Met-1 to Glu-9, Ser-18 to Ile-26.	AR089: 1, AR060: 1, AR033: 1, AR053: 0, AR039: 0, AR096: 0,			103-119

222	HSXFL85	760494	232	69 - 566	1637	Phe-8 to Gly-21.	AR061: 0, AR052: 0, AR104: 0, AR055: 0 H0427: 1 and H0328: 1.		82-107
							AR052: 7, AR096: 6, AR089: 4, AR060: 4, AR053: 4, AR055: 4, AR033: 3, AR104: 2, AR061: 2, AR039: 1 H0251: 5, H0543: 5, H0624: 4, H0170: 4, S0222: 4, H0013: 3, S0003: 3, H0615: 3, H0519: 3, T0049: 2, H0051: 2, H0553: 2, H0131: 2, S0422: 2, S0426: 2, H0659: 2, L0752: 2, S0026: 2, H0171: 1, H0556: 1, H0686: 1, H0650: 1, S0116: 1, H0671: 1, S0376: 1, S0046: 1, H0369: 1, H0497: 1, H0156: 1, H0599: 1, H0042: 1, H0575: 1, S0182: 1, S0049: 1, H0596: 1, H0572: 1, H0015: 1, L0163: 1, S0388: 1, S0051: 1, S6028: 1, H0266: 1, H0328: 1, H0424: 1, H0032: 1, H0673: 1, S0036: 1, H0038: 1, H0040: 1, H0551: 1, T0041: 1, S0210: 1, S0002: 1, H0529: 1, L0763:		

						1, L0807: 1, L0517: 1, H0520: 1, H0660: 1, H0672: 1, S0328: 1, H0696: 1, L0741: 1, L0742: 1, L0439: 1, L0756: 1, L0780: 1, L0731: 1, S0434: 1, S0196: 1 and H0422: 1.				86-105, 40-56
223	HNGDQ71	760510	233	114 - 446	1638		AR055: 2, AR033: 2, AR060: 2, AR061: 1, AR089: 1, AR096: 1, AR052: 0, AR053: 0, AR039: 0, AR104: 0 S0031: 3, H0624: 1, S6026: 1, S0278: 1, S0222: 1, S0051: 1, H0416: 1, H0644: 1, S0052: 1, S0053: 1, S0028: 1, S0032: 1 and S0260: 1.				127-144
224	HTOJT28	760822	234	113 - 550	1639	Trp-30 to Ser-36, Lys-54 to Lys-59, Thr-84 to Asn-89.	AR039: 19, AR053: 9, AR033: 8, AR055: 8, AR096: 7, AR052: 7, AR089: 6, AR060: 6, AR104: 5, AR061: 4 L0740: 8, H0617: 4, L0804: 3, H0068: 2, L0803: 2, H0547: 2, L0747: 2, L0779: 2, H0587: 1, H0581: 1, S0003: 1, H0264: 1, L0649: 1, L0774: 1, L0653:				

225	HSDZF13	760890	235	532-924	1640	Gly-8 to Ser-14.	1, L0655: 1 and L0362: 1. AR061: 9, AR060: 5, AR033: 5, AR052: 5, AR055: 5, AR096: 5, AR104: 5, AR053: 4, AR089: 3, AR039: 0 L0777: 5, S0436: 5, S0116: 3, L0805: 3, L0809: 3, H0696: 3, H0423: 3, S0282: 2, S0354: 2, H0083: 2, H0316: 2, L0763: 2, L0767: 2, L0776: 2, S0406: 2, L0779: 2, S0114: 1, H0657: 1, H0656: 1, S0358: 1, S0444: 1, S0360: 1, H0340: 1, S0046: 1, H0619: 1, H0455: 1, H0333: 1, H0574: 1, H0559: 1, T0109: 1, H0156: 1, L0021: 1, T0074: 1, H0318: 1, S0474: 1, S0049: 1, H0327: 1, H0530: 1, H0615: 1, H0553: 1, H0673: 1, H0708: 1, H0059: 1, L0065: 1, S0438: 1, H0207: 1, S0422: 1, L0520: 1, L0769: 1, L0761: 1, L0521: 1, L0774: 1, L0655: 1, L0659: 1, L0526: 1, L0793: 1, L0666: 1, L0664: 1, H0659: 1, H0518: 1,			91-109, 115-131

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226	HTOBH39	761762	236	47 - 919	1641	Ala-14 to Arg-19, Val-23 to Pro-38, Ser-44 to Gln-53, Pro-69 to Thr-80.		AR053: 21, AR052: 19, AR096: 14, AR055: 13, AR089: 13, AR033: 11, AR060: 9, AR061: 8, AR104: 7, AR039: 3 L0766: 7, L0439: 7, L0752: 4, L0731: 4, L0438: 3, L0748: 2, L0753: 2, S0276: 2, S0430: 1, S0212: 1, S0358: 1, H0637: 1, S0222: 1, H0486: 1, H0042: 1, L0040: 1, S0051: 1, S0214: 1, H0634: 1, H0272: 1, H0100: 1, H0625: 1, H0130: 1, L0773: 1, L0783: 1, L0791: 1, H0666: 1, S3012: 1, L0780: 1 and H0542: 1.		
227	HE9RP73	761860	237	105 - 506	1642	Val-24 to Gly-35, Gly-48 to Ser-59, Ser-123 to Arg-134.		AR061: 5, AR053: 3, AR055: 1, AR052: 1, AR033: 1, AR060: 1, AR089: 1, AR096: 0, AR039: 0, AR104: 0 S0114: 1, H0549: 1 and H0144: 1.			64-82

228	HSXDG07	762023	238	78 - 692	1643	Leu-22 to Asn-32, Leu-34 to Pro-39, Glu-80 to Ser-86.	AR055: 10, AR060: 8, AR052: 7, AR061: 7, AR089: 6, AR053: 5, AR096: 5, AR033: 5, AR104: 4, AR039: 4 L0748: 7, L0439: 4, S0410: 3, L0438: 3, L0756: 3, H0252: 2, L0803: 2, L0666: 2, L0754: 2, H0657: 1, S0360: 1, H0431: 1, H0333: 1, H0014: 1, H0328: 1, L0483: 1, L0142: 1, S0036: 1, H0040: 1, L0598: 1, L0764: 1, L0662: 1, L0794: 1, L0766: 1, L0774: 1, L0653: 1, L0659: 1, L0790: 1, L0352: 1, H0519: 1, L0747: 1, L0749: 1, L0750: 1, L0777: 1, S0192: 1, H0543: 1 and H0423: 1.				111-128, 89-105, 2-18
229	HDPHG57	764498	239	80 - 436	1644	Leu-60 to Asp-68, Ile-75 to Val-82.	AR039: 2, AR033: 1, AR089: 1, AR096: 1, AR055: 1, AR060: 0, AR061: 0, AR053: 0 L0759: 6, L0766: 5, H0052: 4, L0770: 4, L0439: 4, L0740: 4, L0747: 4, H0657: 3, S0358: 3, S0003: 3, L0769: 3, L0754: 3, S0376: 2, H0590: 2, H0040:	6q14	136550, 203310, 269920, 602772		37-57

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230	HGBAD15	765442	240	1220 - 267	1645			1 and H0506: 1. AR096: 1, AR055: 1, AR033: 1, AR089: 1, AR060: 1, AR061: 0, AR052: 0, AR039: 0, AR053: 0, AR104: 0 L0748: 10, L0805: 5, L0750: 3, L0777: 3, H0616: 2, S0422: 2, L0803: 2, L0804: 2, H0520: 2, H0547: 2, H0519: 2, L0744: 2, L0779: 2, L0752: 2, L0731: 2, L0581: 2, S0282: 1, S0360: 1, H0411: 1, H0431: 1, H0042: 1, H0581: 1, H0251: 1, H0596: 1, H0597: 1, H0172: 1, H0123: 1, H0050: 1, H0620: 1, H0014: 1, H0051: 1, L0177: 1, S0003: 1, H0328: 1, H0428: 1, H0553: 1, H0169: 1, H0124: 1, L0378: 1, L0776: 1, L0657: 1, L0791: 1, L0438: 1, H0690: 1, H0521: 1, H0522: 1, L0356: 1, L0439: 1, L0756: 1, L0780: 1, L0753: 1, L0759: 1, S0106: 1 and S0026: 1.			126-142
231	HOEEP07	766074	241	68 -	1646	Asp-3 to Arg-8,		AR096: 18, AR053: 16,			182-199,

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232	HFIHT50	766558	242	19 - 378	1647	Met-1 to Arg-6.	AR096: 2, AR055: 1, AR089: 1, AR060: 1, AR061: 0, AR052: 0, AR053: 0, AR039: 0, AR033: 0, AR104: 0 H0265: 2, L0766: 2, H0656: 1, H0341: 1, H0581: 1, H0634: 1 and S0194: 1.				
233	HANGD38	766868	243	905 - 1387	1648	Ser-42 to Arg-47, Thr-115 to Ser-127, Ser-130 to Trp-136.	AR089: 11, AR096: 11, AR060: 7, AR052: 4, AR053: 3, AR033: 3, AR055: 2, AR061: 1, AR104: 1, AR039: 0 H0024: 3, H0622: 3, H0265: 1, S0358: 1, H0486: 1, H0150: 1, H0050: 1, S0316: 1, H0100: 1, H0144: 1, S0328: 1 and L0743: 1.				55-77, 75-91
234	HPMGQ75	767356	244	299 - 832	1649	Asp-9 to Ile-22, Ser-64 to Leu-69, Thr-91 to Ser-100, Lys-162 to Gln-172.	AR055: 11, AR053: 6, AR060: 6, AR096: 6, AR033: 6, AR061: 6, AR052: 4, AR104: 4, AR089: 4, AR039: 3 H0424: 16, S0380: 13,	22q13.2-q13.31	188826, 250100, 250800, 250800		100-120

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							1650	Tyr-15 to Cys-22.	
							285 - 695		
							245		
							767674		
							HBJJH66		
							235		

236	HEGBB78	768346	246	1022 - 672	1651	Lys-17 to Cys-29, Thr-69 to Cys-79, Arg-92 to Gly-99.	H0539: 1 and L0589: 1. AR033: 8, AR055: 7, AR052: 5, AR053: 4, AR061: 4, AR060: 4, AR089: 4, AR096: 3, AR104: 3, AR039: 0 L0731: 5, L0758: 5, H0620: 3, L0766: 3, S0360: 2, S0002: 2, L0809: 2, L0791: 2, L0748: 2, L0439: 2, L0747: 2, L0601: 2, H0556: 1, S0282: 1, H0125: 1, S0408: 1, H0549: 1, H0550: 1, S0222: 1, H0592: 1, T0114: 1, H0581: 1, H0596: 1, S6028: 1, H0622: 1, H0135: 1, H0087: 1, H0059: 1, H0529: 1, L0769: 1, L0761: 1, L0372: 1, L0646: 1, L0804: 1, L0774: 1, L0776: 1, L0783: 1, L0543: 1, H0670: 1, H0555: 1, S3012: 1, L0757: 1, S0260: 1, L0596: 1 and L0361: 1.			32-55
237	HAJBC01	768776	247	26 - 361	1652		AR039: 2, AR096: 2, AR055: 2, AR104: 1, AR033: 1, AR061: 1, AR089: 0, AR053: 0,				44-92, 1-24, 76-92, 41-57

238	HHGCP75	769003	248	25 - 471	1653	Gly-140 to Glu-149.	AR060: 0, AR052: 0 H0561: 1	7q35-q36	118425, 118425, 118425, 142335, 152427, 163729, 176450, 180105, 190605, 276000, 276000, 600510, 600725	119-137

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239	HAIDO95	771350	249	24 - 1031	1654	Pro-17 to Trp-26, Pro-76 to Arg-81, Asp-99 to Gly-106, Pro-148 to His-157, Glu-178 to Glu-185, Leu-195 to Pro-201.	AR055: 20, AR033: 12, AR053: 11, AR052: 11, AR060: 10, AR089: 10, AR061: 9, AR096: 6, AR104: 3, AR039: 3 L0766: 11, L0769: 3, L0761: 3, L0655: 3, L0777: 3, L0780: 3, H0543: 3, H0556: 2, S0476: 2, H0039: 2, L0794: 2, L0804: 2, L0805: 2, L0787: 2, L0747: 2, L0362: 2, S0026: 2, H0542: 2, L0005: 1, S0356: 1, S0360: 1, H0580: 1, S0132: 1, H0318: 1, L0483: 1, H0032: 1, H0090: 1, H0634: 1, H0538: 1, L0770: 1, L0646: 1, L0771: 1, L5574: 1, L0388: 1, L0653: 1, L0606: 1, L0367: 1, L0789: 1, H0144: 1, H0436: 1, L0749: 1 and S0194: 1.			

240	HE8UD19	771648	250	19 - 759	1655	Lys-20 to Tyr-27, Tyr-35 to Ser-49.	AR096: 3, AR061: 2, AR033: 2, AR060: 1, AR053: 1, AR052: 1, AR055: 0, AR089: 0, AR104: 0 S0414: 5, L0663: 4, L0777: 4, L0803: 3, L0744: 3, L0752: 3, L0731: 3, L0526: 2, L0743: 2, L0740: 2, L0751: 2, L0756: 2, L0758: 2, H0686: 1, S0040: 1, H0650: 1, H0663: 1, H0370: 1, H0013: 1, L0021: 1, S0346: 1, H0251: 1, H0046: 1, S0051: 1, S0318: 1, H0687: 1, H0488: 1, H0412: 1, H0623: 1, H0059: 1, S0002: 1, L0763: 1, L0764: 1, L0766: 1, L0805: 1, L0659: 1, L0664: 1, L0665: 1, H0690: 1, H0435: 1, H0659: 1, H0521: 1, H0522: 1, L0759: 1, S0031: 1, H0543: 1 and S0446: 1.	8q21	124080, 202010, 202010, 214400, 602476, 602667	132-150, 78-94
241	HMAIT58	771900	251	79 - 432	1656	Met-1 to Gly-16, Ser-32 to Lys-38, Ser-64 to Lys-84.	AR096: 17, AR055: 9, AR060: 8, AR039: 7, AR061: 6, AR033: 6, AR052: 6, AR053: 5, AR089: 5, AR104: 4 L0766: 3, S0358: 2, S0278:			36-65

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242	HDAAE77	772217	252	104 - 1435	1657	AR055: 1, AR052: 1, AR053: 1, AR061: 1, AR089: 1, AR033: 1, AR104: 1, AR060: 1, AR096: 0, AR039: 0 L0439: 4, H0013: 2, H0497: 1, T0010: 1, T0041: 1, H0144: 1 and L0438: 1.			71-89, 19-44
243	HKAOJ07	772639	253	112 - 423	1658	AR096: 8, AR089: 6, AR052: 5, AR053: 5, AR039: 4, AR033: 3, AR060: 2, AR104: 2, AR055: 2, AR061: 1 L0750: 4, H0265: 3, L0794: 3, L0731: 3, H0635: 2, H0494: 2, L0766: 2, S0116: 1, H0052: 1, H0264: 1, S0002: 1, L0769: 1, L0764: 1, L0768: 1, H0144: 1, L0608: 1 and L0601: 1.			
244	HDTFC73	772840	254	983 -	1659	Leu-19 to Asn-29,	AR052: 2, AR053: 2,			28-58

				1303	Glu-96 to Lys-101.	AR096: 1, AR089: 1, AR055: 1, AR104: 1, AR061: 1, AR033: 1, AR060: 1 L0439: 7, L0777: 3, S0007: 2, H0031: 2, L0438: 2, L0411: 1, H0662: 1, H0638: 1, S0222: 1, H0486: 1, L0021: 1, H0052: 1, T0010: 1, H0032: 1, H0268: 1, L0351: 1, L0766: 1, L0804: 1, L0655: 1, L0809: 1, S0216: 1 and H0522: 1.			44-60, 129-145
245	HDTFI32	773040	255	74 - 538	1660	Pro-13 to Ser-18.	AR096: 2, AR089: 2, AR104: 1, AR060: 1, AR052: 1, AR033: 0, AR039: 0, AR061: 0 S0476: 11, H0556: 10, H0265: 4, H0635: 4, H0657: 2, H0638: 2, S0132: 2, H0036: 2, L0601: 2, H0423: 2, H0713: 1, S0134: 1, S0298: 1, H0486: 1, H0069: 1, H0575: 1, T0082: 1, H0581: 1, L0471: 1, H0321: 1, H0591: 1, H0560: 1, H0641: 1, L0506: 1, L0775: 1, L0657: 1, H0435: 1, H0518: 1, H0521: 1, S0406: 1, L0749: 1 and H0543: 1.			

246	HLQCY70	773347	256	47 - 373	1661	Gly-5 to Gln-12, Lys-98 to Pro-106.	AR033: 46, AR055: 45, AR039: 38, AR053: 35, AR089: 34, AR052: 33, AR096: 26, AR061: 21, AR060: 21, AR104: 19 H0617: 9, L0751: 6, L0750: 5, L0752: 5, L0770: 4, L0747: 4, L0761: 3, L0775: 3, H0657: 2, S0358: 2, S0444: 2, H0457: 2, H0188: 2, H0181: 2, H0606: 2, L0769: 2, L0772: 2, L0764: 2, L0766: 2, L0774: 2, L0742: 2, L0748: 2, L0757: 2, L0758: 2, H0624: 1, H0685: 1, H0295: 1, S0114: 1, H0661: 1, S0140: 1, H0411: 1, S0278: 1, H0549: 1, H0587: 1, H0574: 1, H0013: 1, H0253: 1, H0318: 1, H0052: 1, H0309: 1, H0204: 1, H0545: 1, H0033: 1, H0424: 1, H0598: 1, H0135: 1, H0163: 1, H0616: 1, H0412: 1, H0059: 1, H0494: 1, H0560: 1, S0440: 1, S0144: 1, L5565: 1, L0373: 1, L0646: 1, L0768: 1, L0499: 1, L0497: 1, L0513: 1, L0783: 1,		48-64, 72-88

						L0384: 1, L0519: 1, L3872: 1, L0368: 1, L0665: 1, S0053: 1, H0144: 1, H0670: 1, H0672: 1, H0651: 1, H0696: 1, S0406: 1, L0740: 1, L0754: 1, L0780: 1, L0731: 1, L0596: 1, S0026: 1, H0543: 1, H0677: 1 and H0352: 1.			61-77
247	HELDG78	773740	257	2 - 301	1662	Lys-31 to Lys-39, Gln-41 to Lys-46, Pro-79 to Ala-85, Glu-95 to Leu-100.	AR055: 5, AR052: 3, AR061: 3, AR033: 3, AR060: 2, AR089: 2, AR039: 2, AR104: 2, AR053: 1, AR096: 1 S0045: 1, S0222: 1, H0250: 1, H0617: 1 and S0028: 1.			
248	HAGEK19	774276	258	649 - 41	1663		AR033: 13, AR104: 10, AR055: 7, AR060: 5, AR061: 5, AR052: 5, AR096: 4, AR089: 4, AR053: 3, AR039: 2 S0010: 4, S0222: 3, H0455: 2, L0803: 2, L0439: 2, L0745: 2, S0282: 1, S0400: 1, H0722: 1, H0456: 1, H0441: 1, S0346: 1, H0714: 1, H0509: 1, L0769: 1, L0793: 1, L0438: 1,			144-160, 99-115

249	H2CBA34	774569	259	291 - 854	1664	Asp-20 to Leu-26, Gln-55 to Thr-60, Asn-74 to Asn-86.	L0756: 1, S0434: 1 and S0106: 1.				114-130, 147-163
							AR055: 11, AR033: 9, AR060: 6, AR104: 6, AR096: 6, AR061: 5, AR089: 4, AR053: 4, AR052: 4, AR039: 3 L0740: 2, S0222: 1, T0082: 1, T0110: 1, T0010: 1, L0483: 1, L0763: 1, L0639: 1, L0747: 1, L0777: 1, L0758: 1 and L0599: 1.				
250	HDPTC79	774739	260	465 - 764	1665		AR052: 8, AR053: 7, AR033: 3, AR055: 3, AR096: 3, AR089: 2, AR061: 2, AR060: 2, AR104: 1, AR039: 0 L0777: 5, L0439: 2, L0596: 2, T0004: 1, L0658: 1, H0518: 1, H0521: 1, L0731: 1 and S0106: 1.				60-78, 17-33
251	HTHBY73	775247	261	273 - 734	1666	Met-1 to Arg-7.	AR055: 17, AR033: 13, AR039: 12, AR052: 10, AR089: 10, AR053: 10, AR061: 9, AR060: 8, AR096: 7, AR104: 7 H0063: 1				90-116, 51-70, 79-95, 21-37
252	HE8DL19	775419	262	152 - 592	1667	Gln-11 to Arg-21.	AR055: 2, AR089: 1, AR104: 1, AR060: 1,				44-65, 92-112, 21-

253	HMEGB46	775455	263	31 - 423	1668	Leu-12 to Thr-19, Arg-25 to Glu-39, Glu-41 to Cys-48, Ser-65 to Ser-71, Pro-84 to Gly-89, Ser-97 to Arg-103.	AR096: 0, AR061: 0, AR033: 0, AR053: 0, AR039: 0, AR052: 0 H0013: 1, S0214: 1, H0615: 1 and L0544: 1.		37, 124-140
							AR055: 7, AR052: 5, AR096: 5, AR060: 4, AR053: 3, AR033: 3, AR089: 3, AR104: 3, AR061: 3, AR039: 2 L0766: 8, L0777: 7, L0794: 5, L0770: 4, H0266: 3, L0803: 3, L0776: 3, H0144: 3, L0740: 3, L0754: 3, L0750: 3, S0222: 2, S0414: 2, H0013: 2, H0575: 2, H0590: 2, H0644: 2, L0769: 2, L0764: 2, L0662: 2, L0809: 2, L0789: 2, H0696: 2, L0439: 2, L0745: 2, S0026: 2, H0170: 1, H0556: 1, H0685: 1, H0713: 1, S0045: 1, H0411: 1, H0497: 1, L0021: 1, H0004: 1, H0052: 1, L0041: 1, H0083: 1, H0267: 1, H0615: 1, H0598: 1, H0591: 1, H0412: 1, H0560: 1, H0641: 1, L0796: 1, L0761: 1, L0771: 1, L0804: 1, L0775:		102-131

						1, L0375: 1, L0806: 1, L0805: 1, L0659: 1, L0788: 1, L0666: 1, H0520: 1, H0660: 1, H0521: 1, H0522: 1, S0406: 1, H0555: 1, S0028: 1, L0747: 1, S0031: 1, L0608: 1, L0593: 1, H0668: 1, S0242: 1 and H0423: 1.			349-366, 272-288, 380-396
254	HTEIA85	778081	264	125 - 1657	1669	Val-29 to Asp-34, Gln-78 to Gln-86, Val-94 to Leu-100, Glu-112 to Leu-117, Gln-119 to Ile-133, Glu-152 to Ala-157, Thr-159 to Gln-168, Lys-209 to Glu-218, Thr-225 to Ser-231, Trp-410 to Trp-415, Ala-505 to Ser-510.	AR055: 6, AR052: 6, AR053: 5, AR033: 4, AR060: 4, AR089: 4, AR061: 3, AR096: 3, AR104: 2, AR039: 2 L0748: 11, L0758: 11, L0594: 6, L0439: 5, L0759: 5, H0556: 4, L0769: 4, S0442: 3, H0036: 3, H0083: 3, H0124: 3, H0100: 3, L0662: 3, L0666: 3, L0756: 3, L0752: 3, H0170: 2, S0045: 2, H0644: 2, H0628: 2, H0038: 2, H0551: 2, L0564: 2, S0422: 2, L0770: 2, L0646: 2, L0771: 2, L0766: 2, L0649: 2, L0653: 2, L0659: 2, H0539: 2, L0740: 2, L0747: 2, L0749: 2, L0753: 2, L0757: 2, S0436: 2, L0584: 2, L0599:			

												73-97,
255	HSHBF13	778087	265	270 -	1670	Ala-18 to Gln-28.	AR052: 16, AR055: 16, 2, L0595: 2, H0686: 1, S0040: 1, H0295: 1, S0212: 1, H0255: 1, H0661: 1, S0444: 1, S0360: 1, H0580: 1, H0729: 1, S0046: 1, L0717: 1, S0278: 1, S0222: 1, H0587: 1, H0333: 1, H0427: 1, H0156: 1, H0575: 1, H0004: 1, H0253: 1, H0545: 1, H0046: 1, H0045: 1, H0051: 1, S0388: 1, H0594: 1, H0428: 1, H0673: 1, H0169: 1, H0674: 1, H0135: 1, H0040: 1, H0268: 1, L0351: 1, T0041: 1, S0382: 1, S0306: 1, S0440: 1, H0509: 1, S0144: 1, S0426: 1, H0743: 1, L0369: 1, L0638: 1, L0764: 1, L0765: 1, L0768: 1, L0388: 1, L0774: 1, L0657: 1, L5623: 1, L0790: 1, L0663: 1, L0664: 1, H0144: 1, L0438: 1, H0519: 1, H0648: 1, H0521: 1, H0522: 1, S0013: 1, H0436: 1, S3014: 1, S0027: 1, L0751: 1, L0779: 1, H0543: 1 and L0600: 1.			

				707			AR053: 14, AR033: 12, AR060: 10, AR089: 8, AR096: 7, AR061: 7, AR104: 5, AR039: 4 H0046: 6, L0758: 5, L0794: 3, L0803: 3, L0779: 3, H0052: 2, H0424: 2, H0135: 2, L0809: 2, L0789: 2, H0690: 2, S3014: 2, L0743: 2, L0751: 2, L0731: 2, H0295: 1, S0001: 1, S0282: 1, H0484: 1, H0306: 1, S0360: 1, S0278: 1, S6022: 1, H0457: 1, H0031: 1, H0316: 1, H0038: 1, S0002: 1, L0800: 1, L0643: 1, L0764: 1, L0773: 1, L0650: 1, L0774: 1, L0655: 1, L0658: 1, L0659: 1, L0664: 1, L0665: 1, H0547: 1, H0435: 1, H0670: 1, S0037: 1, L0748: 1, L0599: 1 and L0601: 1.			108-134, 42-58
256	HLYCQ80	778291	266	539 - 240	1671	Lys-31 to Thr-39.	AR053: 1, AR060: 1, AR055: 1, AR033: 1, AR061: 0, AR089: 0, AR096: 0, AR052: 0, AR039: 0, AR104: 0 L0758: 13, L0756: 3, L0752: 3, L0438: 2, H0176:			52-72, 7-23

							1, H0261: 1, H0309: 1, H0081: 1, H0029: 1, H0038: 1, H0616: 1, H0202: 1, L0369: 1, L0766: 1, L0774: 1, L0776: 1, L0635: 1, L0809: 1, L0791: 1, H0547: 1, H0711: 1, H0690: 1, S0152: 1, H0479: 1, L0743: 1, L0439: 1, L0750: 1, L0777: 1, L0755: 1, H0445: 1 and L0588: 1.			
257	HE2OF81	778504	267	162 - 611	1672	Met-1 to Gln-8, Leu-17 to Leu-29, Gln-109 to Thr-115.	AR055: 13, AR060: 9, AR052: 9, AR061: 8, AR053: 8, AR033: 5, AR089: 4, AR096: 3, AR104: 2, AR039: 0 L0761: 3, L0439: 3, L0747: 3, L0766: 2, H0659: 2, L0779: 2, L0777: 2, H0170: 1, S0360: 1, H0550: 1, H0023: 1, H0018: 1, H0641: 1, L0763: 1, L0769: 1, L0764: 1, L0803: 1, L0774: 1, L0655: 1, L0666: 1, H0648: 1 and H0436: 1.			91-107
258	HTEBB88	779291	268	52 - 630	1673	Glu-53 to Asp-58, Trp-98 to Lys-103, Leu-131 to Arg-144.	AR052: 285, AR089: 170, AR096: 161, AR053: 143, AR060: 83, AR104: 64, AR033: 49, AR039: 43,			103-120

259	HWHGD82	779607	269	81 - 461	1674	Asn-14 to Ser-19, Asp-46 to Phe-51, Glu-101 to Asp-117, Ile-121 to Gly-127.	AR039: 23, AR104: 18, AR033: 17, AR096: 10, AR052: 8, AR053: 7, AR055: 6, AR089: 6, AR060: 5, AR061: 4 L0754: 16, H0617: 8, S0360: 6, H0551: 6, L0748: 6, L0750: 6, H0543: 6, L0766: 5, L0666: 5, L0751: 5, L0747: 5, S0418: 4, H0553: 4, L0665: 4, H0542: 4, H0586: 3, S0414: 3, H0264: 3, H0494: 3, S0344: 3, L0769: 3, L0438: 3, H0547: 3, H0519: 3, H0521: 3, L0740: 3, L0757: 3, S0192: 3, H0656: 2, H0254: 2, H0255: 2, S0046: 2, S0132: 2, H0587: 2, H0559: 2, H0618: 2, H0620: 2, H0199: 2, H0688: 2, L0770: 2, L0372: 2, L0642: 2, L0771: 2, L0662: 2, L0653: 2, L0659: 2, L0783: 2, H0435: 2, H0660: 2, L0602: 2, H0436: 2, S3014: 2, L0731: 2, L0759: 2, L0588:	AR061: 42, AR055: 40 L0758: 6, H0616: 3, H0038: 2 and H0618: 1.	13q12	121011, 121011, 129500, 253700, 601885, 602221	18-44, 75-96

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						1, L0663: 1, S0428: 1, H0144: 1, H0593: 1, S0126: 1, H0690: 1, H0670: 1, S0328: 1, S0380: 1, S0350: 1, H0522: 1, S0188: 1, S0027: 1, S0206: 1, L0744: 1, L0439: 1, L0756: 1, L0777: 1, L0755: 1, H0445: 1, H0136: 1, S0042: 1 and L0697: 1.			102-119
260	HWADH67	779663	270	143 - 628	1675	Glu-37 to Asn-44.	AR052: 5, AR053: 3, AR096: 3, AR033: 3, AR089: 2, AR060: 2, AR104: 2, AR061: 1, AR055: 0, AR039: 0 L0439: 7, L0759: 5, H0624: 4, H0170: 4, S0003: 4, L0766: 4, H0657: 3, H0013: 3, L0438: 3, H0068: 2, L0598: 2, L0646: 2, L0794: 2, L0659: 2, L0647: 2, L0666: 2, H0520: 2, L0747: 2, L0756: 2, L0779: 2, L0777: 2, L0588: 2, L0592: 2, H0171: 1, H0556: 1, S0376: 1, S0045: 1, S0222: 1, H0586: 1, T0114: 1, H0581: 1, L0471: 1, H0355: 1, S6028: 1, S0214: 1, H0615: 1, H0428: 1,			

							H0039: 1, H0591: 1, H0040: 1, T0004: 1, L0763: 1, L0768: 1, L0774: 1, L0806: 1, L0789: 1, L0663: 1, L0665: 1, L0352: 1, H0519: 1, H0690: 1, H0648: 1, H0518: 1, H0521: 1, L0780: 1, L0753: 1, L0755: 1, L0731: 1, L0758: 1, L0596: 1, L0599: 1, L0593: 1, S0026: 1, H0667: 1 and H0543: 1.			86-110, 7-32, 65-82
261	HKADC82	779838	271	138 - 530	1676	Asn-3 to Phe-9.	AR052: 3, AR033: 2, AR104: 2, AR089: 2, AR055: 2, AR039: 2, AR096: 2, AR053: 2, AR061: 1, AR060: 1 L0766: 5, H0494: 2, L0755: 2, L0800: 1, L0773: 1 and L0777: 1.			99-121, 124-140
262	HHESK83	780458	272	29 - 457	1677	Met-1 to Glu-10.	AR052: 3, AR053: 2, AR104: 2, AR089: 1, AR033: 1, AR061: 1, AR060: 1, AR096: 1, AR055: 0, AR039: 0 H0543: 1			60-77, 22-38
263	HMIAT16	780804	273	822 - 502	1678	Pro-89 to Phe-96.	AR033: 20, AR104: 16, AR055: 8, AR061: 7, AR060: 5, AR053: 5,			

264	HSLJK83	780819	274	149 - 763	1679	Asp-39 to Gln-44.	AR052: 5, AR089: 5, AR096: 4, AR039: 3 S0414: 3, S0036: 3, L0439: 3, H0327: 2, H0051: 2, S6028: 2, S0282: 1, H0406: 1, H0438: 1, S0010: 1, S0038: 1, S0260: 1 and S0412: 1.			9-29, 120-136
265	HADFW62	781376	275	29 - 340	1680	Pro-37 to Cys-42, Pro-52 to Gly-63.	AR052: 3, AR096: 3, AR053: 2, AR089: 2, AR033: 2, AR039: 1, AR060: 1, AR104: 1, AR055: 1, AR061: 0 L0439: 2, L0747: 2, L0756: 2, H0556: 1, S0116: 1, H0333: 1, H0427: 1, H0156: 1, H0052: 1, S0210: 1, L0769: 1, L0646: 1, L0657: 1, L0384: 1, L0543: 1, H0670: 1, H0521: 1, H0478: 1, L0745: 1, L0749: 1, L0757: 1 and L0591: 1.			77-95, 10-26
266	HDTBV64	781623	276	24 - 401	1681	Ile-35 to Ser-44.	AR033: 8, AR060: 6,				80-102, 1-

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AR089: 3, AR096: 3, AR052: 2, AR053: 2, AR061: 1, AR104: 1, AR055: 0, AR039: 0 L0752: 8, L0766: 6, S0444: 5, L0770: 5, L0439: 5, L0731: 5, S0360: 3, H0031: 3, L0803: 3, S0126: 3, L0755: 3, L0758: 3, S0358: 2, H0722: 2, H0090: 2, H0056: 2, L0805: 2, L0659: 2, L0666: 2, L0665: 2, H0519: 2, S0330: 2, H0521: 2, L0747: 2, H0170: 1, H0716: 1, H0740: 1, S0114: 1, S0212: 1, S0442: 1, S0354: 1, H0580: 1, H0329: 1, H0431: 1, H0497: 1, H0331: 1, H0574: 1, H0632: 1, H0486: 1, H0427: 1, L0021: 1, H0036: 1, H0274: 1, S0010: 1, H0318: 1, H0581: 1, H0374: 1, H0052: 1, H0596: 1, H0597: 1, H0545: 1, H0373: 1, S0388: 1, H0107: 1, S0003: 1, S0214: 1, H0428: 1, H0622: 1, H0553: 1, H0163: 1, H0087: 1, T0067: 1, H0494: 1, H0560: 1, S0438:								

						1, S0440: 1, S0426: 1, UNKWN: 1, L0598: 1, L0763: 1, L0769: 1, L0638: 1, L0761: 1, L0641: 1, L0776: 1, L0379: 1, L0657: 1, L0809: 1, L0519: 1, L0791: 1, L0663: 1, H0684: 1, H0672: 1, S0378: 1, H0522: 1, S0404: 1, S0406: 1, S0028: 1, L0750: 1, L0756: 1, L0753: 1, S0031: 1, H0445: 1, H0595: 1, S0436: 1, L0581: 1, L0608: 1, S0011: 1, S0026: 1, S0192: 1, S0196: 1, H0423: 1 and S0424: 1.		55-78, 31-48
267	HOHBR65	781821	277	225 - 578	1682	Met-1 to Gly-7, Pro-99 to Phe-104.	AR096: 1, AR052: 1, AR033: 1, AR060: 1, AR089: 1, AR061: 0, AR055: 0, AR053: 0, AR104: 0 H0009: 2, H0583: 1, S0045: 1 and S0250: 1.			207-223
268	HRABZ84	782028	278	119 - 901	1683	Glu-46 to Asn-51, Gly-56 to Gly-63.	AR096: 6, AR053: 6, AR052: 4, AR089: 3, AR060: 2, AR039: 2, AR033: 2, AR055: 2, AR104: 2, AR061: 1 L0740: 8, L0749: 8,			

S0040: 4, L0766: 4, L0779: 4, L0471: 3, H0090: 3, H0040: 3, L0748: 3, L0752: 3, S0358: 2, H0644: 2, H0616: 2, L0763: 2, L0774: 2, L0659: 2, L0809: 2, H0144: 2, L0744: 2, L0754: 2, L0750: 2, L0777: 2, L0758: 2, H0686: 1, H0685: 1, H0583: 1, H0657: 1, H0662: 1, S0360: 1, S0046: 1, L0717: 1, H0351: 1, H0549: 1, H0586: 1, H0587: 1, H0013: 1, S0280: 1, H0156: 1, H0575: 1, H0318: 1, H0231: 1, H0046: 1, S6028: 1, H0266: 1, H0687: 1, S0003: 1, S0214: 1, H0063: 1, H0264: 1, H0641: 1, S0002: 1, S0426: 1, L0764: 1, L0662: 1, L0386: 1, L0775: 1, L0654: 1, L0665: 1, L0438: 1, H0519: 1, H0593: 1, H0365: 1, H0555: 1, L0439: 1, L0746: 1, L0747: 1, L0756: 1, L0780: 1, L0755: 1, S0308: 1, L0591: 1, L0362: 1, L0366: 1, S0026: 1, S0192: 1 and H0506: 1.							

269	HKABD18	782431	279	30 - 338	1684	Met-1 to Pro-6, Thr-18 to Ala-32, Gln-39 to Gly-44.	AR089: 47, AR096: 47, AR104: 33, AR053: 25, AR039: 23, AR052: 22, AR033: 22, AR060: 17, AR055: 4, AR061: 3 L0803: 2, L0748: 2, H0556: 1, S0134: 1, H0734: 1, S0010: 1, H0687: 1, H0428: 1, H0494: 1, L0662: 1, L0804: 1, L0776: 1, L0809: 1, L0787: 1, S0152: 1, H0522: 1, L0439: 1, L0756: 1, L0752: 1, L0758: 1, L0599: 1, L0601: 1 and H0543: 1.			51-67
270	HUFAJ06	783017	280	231 - 1040	1685	Met-1 to Arg-7, Pro-9 to Ile-17, Glu-26 to Tyr-38.	AR052: 5, AR053: 3, AR096: 2, AR089: 1, AR033: 1, AR055: 1, AR104: 1, AR060: 1, AR061: 1, AR039: 0 L0439: 5, L0770: 4, L0794: 4, L0758: 4, L0665: 3, H0657: 2, S0360: 2, H0039: 2, H0040: 2, H0551: 2, L0803: 2, L0747: 2, L0777: 2, H0423: 2, H0638: 1, S0420: 1, S0007: 1, H0050: 1, H0510: 1, H0594: 1, S0003: 1, H0264: 1, H0494: 1, H0560: 1, H0625:			45-61

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271	HDQFV46	783316	281	77 - 667	1686	His-13 to Gln-20, Gly-27 to Ser-55, Glu-175 to Gly-187.	AR052: 51, AR033: 42, AR055: 40, AR053: 36, AR089: 30, AR060: 14, AR061: 12, AR096: 11, AR039: 10, AR104: 6				
272	HMEKH64	783318	282	139 - 1155	1687	Leu-26 to Gly-33, Glu-44 to Cys-49, Gln-54 to Ile-62, Glu-75 to Lys-80.	AR033: 3, AR052: 3, AR089: 3, AR060: 3, AR053: 2, AR096: 2, AR055: 1, AR039: 1, AR104: 1, AR061: 1 L0766: 12, H0659: 5, L0749: 5, S0410: 4, S0422: 4, H0650: 3, H0341: 3, H0032: 3, H0529: 3, L0646: 3, H0520: 3, H0547: 3, H0521: 3, L0748: 3, H0423: 3, H0657: 2, S0280: 2, H0266: 2, H0090: 2, H0040: 2, L0803: 2, L0804: 2, L0666: 2, H0658: 2, H0672: 2, L0756: 2, L0757: 2,			300-316, 176-192

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								L0759: 2, S0424: 2, H0170: 1, H0556: 1, H0656: 1, S0001: 1, H0662: 1, S0418: 1, S0420: 1, S0444: 1, H0728: 1, S0045: 1, L0717: 1, H0486: 1, H0318: 1, H0596: 1, T0110: 1, H0024: 1, H0428: 1, H0616: 1, H0551: 1, H0560: 1, H0625: 1, S0440: 1, H0647: 1, L0520: 1, L0763: 1, L0764: 1, L0521: 1, L0774: 1, L0375: 1, L0805: 1, L0776: 1, L0655: 1, L0635: 1, L0809: 1, L0789: 1, L0663: 1, L0665: 1, S0374: 1, H0519: 1, H0435: 1, H0670: 1, H0134: 1, S0406: 1, H0555: 1, L0439: 1, L0750: 1, L0777: 1, L0752: 1, L0755: 1, L0758: 1, L0608: 1, H0542: 1 and H0422: 1.
273	HTLEE85	783631	283	51 - 413	1688	Gln-77 to Ala-82, Thr-90 to Asp-100, Leu-108 to Ala-120.	AR039: 10, AR055: 8, AR033: 7, AR053: 7, AR089: 6, AR052: 6, AR096: 5, AR060: 5, AR104: 5, AR061: 4 H0618: 3, H0052: 2, H0411: 1, H0333: 1, H0253: 1, H0622: 1, H0424: 1,			

							S0378: 1, L0749: 1 and S0436: 1.			
274	HCE4Q82	783713	284	73 - 795	1689	Gly-10 to Arg-18, Leu-23 to Lys-30, Gly-53 to Pro-60, Asn-72 to Arg-81, Ser-86 to Lys-95, Glu-97 to Asp-105.	AR104: 12, AR096: 11, AR053: 10, AR055: 10, AR052: 9, AR060: 8, AR033: 7, AR089: 7, AR061: 5, AR039: 5 H0038: 5, H0616: 5, L0758: 5, S0003: 3, L0741: 3, S0278: 2, H0156: 2, H0052: 2, S0144: 2, S0344: 2, L0768: 2, S0218: 1, H0484: 1, H0638: 1, S0045: 1, S0046: 1, H0438: 1, H0562: 1, L0769: 1, L0794: 1, S0122: 1 and L0749: 1.			170-186, 120-136
275	HODEC95	783883	285	29 - 382	1690		AR055: 8, AR052: 7, AR089: 6, AR060: 6, AR096: 5, AR033: 5, AR104: 5, AR053: 4, AR039: 4, AR061: 4 H0615: 4 and H0556: 1.			67-89, 91-107
276	HCBBA47	783892	286	1035 - 1340	1691	Thr-37 to Ser-43, Pro-62 to Asn-67, His-73 to Tyr-82, Pro-94 to Ser-102.	AR104: 240, AR061: 184, AR060: 129, AR033: 121, AR089: 99, AR053: 77, AR052: 76, AR055: 67, AR039: 62, AR096: 56 S0136: 8, L0754: 5, L0758: 5, L0768: 3, L0766:			40-62, 19-35

277	HSKEQ61	783939	287	577 - 2247	1692	Met-1 to Lys-6, Ser-31 to Ala-45, Cys-102 to Glu-107, Arg-151 to Asp-157, Gln-191 to Ser-197, Glu-215 to Leu-220, Ser-264 to Leu-270,	AR052: 26, AR033: 26, AR053: 18, AR089: 15, AR060: 9, AR096: 9, AR055: 8, AR104: 6, AR061: 5, AR039: 4 H0266: 4, H0547: 4, H0521: 3, L0748: 3, S0358: 3, L0803: 3, L0749: 3, H0506: 3, H0560: 2, L0598: 2, L0662: 2, L0794: 2, L0804: 2, L0805: 2, H0520: 2, H0547: 2, H0436: 2, L0747: 2, L0755: 2, L0685: 2, H0583: 1, H0650: 1, H0177: 1, S0358: 1, H0580: 1, S0222: 1, H0642: 1, T0060: 1, H0421: 1, S0388: 1, H0266: 1, H0687: 1, T0023: 1, H0553: 1, H0379: 1, H0268: 1, S0144: 1, S0422: 1, H0529: 1, L0520: 1, L0761: 1, L0667: 1, L0772: 1, L0764: 1, L0652: 1, L0664: 1, L0665: 1, H0144: 1, H0519: 1, S0126: 1, H0672: 1, H0521: 1, L0746: 1, L0750: 1, L0779: 1, L0731: 1, L0759: 1, L0601: 1, L0603: 1, S0196: 1, H0543: 1 and H0423: 1.	9q31.2	223900, 253800, 253800	517-533, 476-492